



# ***STIC Search Report***

## ***Biotech-Chem Library***

**STIC Database Tracking Number: 96364**

**TO: Daniel Sullivan  
Location: CM1/12D12/11E12  
Art Unit: 1636  
Wednesday, June 25, 2003**

**Case Serial Number: 982091**

**From: Edward Hart  
Location: Biotech-Chem Library  
CM1-6B02  
Phone: 305-9203**

**edward.hart@uspto.gov**

### **Search Notes**

Examiner Sullivan,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



# STIC SEARCH RESULTS

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor  
308-4258, CM1-1E01

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library, CM1-1E01 Desk



## CDS

precursor cells treated 2-weeks mitotic inhibitor after 5-weeks retinoic acid (RA) induction. -majorly NR2 neuron\* 489..1178

/note="unnamed protein product"

/codon\_start=1

/protein\_id="BAC04755.1"

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BASE COUNT 658 a 716 c 907 g 653 t

## ORIGIN

Query Match 1.7%: Score 484; DB 9; Length 2934;  
Best Local Similarity 100.0%; Pred. No. 1.3e-239;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 25614 AGCAGCAGACAGAGCCCGCGCTACCGCCTTAGGGGTTTCCCGCGGTTGGGAAAGCCAT 25673
DB 1 AGCAGCAGACAGAGCCCGCGCTACCGCCTTAGGGGTTTCCCGCGGTTGGGAAAGCCAT 60
OY 25674 TGAGAGATTAAAGCCCGGAGGTGTGACTAATCAAGATTTCATTGAAATGCGACGGTG 25733
DB 61 TGAGAGATTAAAGCCCGGAGGTGTGACTAATCAAGATTTCATTGAAATGCGACGGTG 120
OY 25734 TCTGAGCAGAGGCTAAGTGTAGGAGAGGCGGAGGAAATGCAATAGAGAGACAGCGG 25793
DB 121 TCTGAGCAGAGGCTAAGTGTAGGAGAGGCGGAGGAAATGCAATAGAGAGACAGCGG 180
OY 25794 ACCTGGAAGGCTGGCTCAACCGCGCCCGCGGCGGAGCGGTTCCGCGCAGAGGG 25853
DB 181 ACCTGGAAGGCTGGCTCAACCGCGCCCGCGGCGGAGCGGTTCCGCGCAGAGGG 240
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DB 361 GCCCGGACCGACGCGTGGAGCGCGGAGACCGCCAGCGGCGGAGAAACCGCCAGCGGGA 420
OY 26034 CTAGACACACACAGCGCGCGGCGGAGACGAGACCGAGCGCGGAGCGGCGCTCTAC 26093
DB 421 CTAGACACACACAGCGCGCGGCGGAGACGAGACCGAGCGCGGAGCGGCGCTCTAC 480
OY 26094 GCCG 26097
DB 481 GCCG 484

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## RESULT 5

BC026909 2579 bp mRNA linear PRI 08-APR-2002  
LOCUS BC026909 IMAGE:4932944, mRNA, complete cds.

DEFINITION Homo sapiens, hypothetical gene LOC127703, clone MGC:24981

ACCESSION BC026909

VERSION BC026909.1 GI:20071213

KEYWORDS MGC.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 2579)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer

## REMARK

COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgaphs-remail.nih.gov](mailto:cgaphs-remail.nih.gov)  
Tissue Procurement: David N. Louis, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunnar, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 29 Row: n Column: 8  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

## FEATURES

location/Qualifiers

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## CDS

BASE COUNT 605 a 598 c 771 g 605 t  
ORIGIN

Query Match 1.3%: Score 361; DB 9; Length 2579;  
Best Local Similarity 100.0%; Pred. No. 1.1e-175;  
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 28477 GCTAGATGTTCCGATCCAGGCTACCTGAGGGGGCCAAATTCCTGGGGACCCAC 28536
DB 115 GCTAGATGTTCCGATCCAGGCTACCTGAGGGGGCCAAATTCCTGGGGACCCAC 174
OY 28537 CTCCTGATTATGTCACCGCCAGCTCCACAGCAGCACTCACTCATGCGCAAGTC 28596
DB 175 CTCCTGATTATGTCACCGCCAGCTCCACAGCAGCACTCACTCATGCGCAAGTC 234
OY 28597 CCAAGATGCTTAACGAGAAATTGGCATGGATGCGAGCAGAGTGAACCTATCTGAGA 28656
DB 235 CCAAGATGCTTAACGAGAAATTGGCATGGATGCGAGCAGAGTGAACCTATCTGAGA 294
OY 28657 GGAAGTCTCTGTAGTACACCTCTGACAAACCAACCTTCACAGGCGCTGATCCCTGAGG 28716
DB 295 GGAAGTCTCTGTAGTACACCTCTGACAAACCAACCTTCACAGGCGCTGATCCCTGAGG 354
OY 28717 AAGGGTGCACACCCCGCAGAGGGGACAGATTCCCGGCGCTGAGCCTGAGAAACATGG 28776
DB 355 AAGGGTGCACACCCCGCAGAGGGGACAGATTCCCGGCGCTGAGCCTGAGAAACATGG 414
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ORIGIN		
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Best Local Similarity	99.94;	Pred. No. 0;
Matches 1286; Conservative	0;	Mismatches 0; Indels 1; Gaps 1;
QY	1	ATATGATCCAGCAATTTCACTTCTTAGTCTGTACCCAAAAAGTGAAAGCAGGACTTGA 60
DB	62528	ATATGATCCAGCAATTTCACTTCTTAGTCTGTACCCAAAAAGTGAAAGCAGGACTTGA 62587
QY	61	ACAGATATTTGGACCCCATGTTTCAAGCAGCANTATTACACAGTAGTAGTCAAAACATG 120
DB	62588	ACAGATATTTGGACCCCATGTTTCAAGCAGCANTATTACACAGTAGTAGTCAAAACATG 62647
QY	121	AAAGCGACCTATCTTTATTGGCAAAATGAATGGTAAACAAATTCGGGTATATATGCAAG 180
DB	62648	AAAGCGACCTATCTTTATTGGCAAAATGAATGGTAAACAAATTCGGGTATATATGCAAG 62707
QY	181	GAATATTCAACTTTAAATGGAATTTCTGGCTGGCATGTGGCTCACACGTGTATATCCCA 240
DB	62708	GAATATTCAACTTTAAATGGAATTTCTGGCTGGCATGTGGCTCACACGTGTATATCCCA 62767
QY	241	ACACTTTGGGTGGCTGAGTGGCGCATCACTTTGAGCTCAGAGTTTGAGACCGCTGG 300
DB	62768	ACACTTTGGGTGGCTGAGTGGCGCATCACTTTGAGCTCAGAGTTTGAGACCGCTGG 62827
QY	301	ATAATATGGCAAAACCCCATCCCTATATAAAAAATACTAAAAATTAAGCTAGGCTGGCG 360
DB	62828	ATAATATGGCAAAACCCCATCCCTATATAAAAAATACTAAAAATTAAGCTAGGCTGGCG 62887
QY	361	GCAGTACCAGCTATTTCAGGGGGCTGAGTGGGAGAAATTCCTTGAGCCCTGGGAGTCAATG 420
DB	62888	GCAGTACCAGCTATTTCAGGGGGCTGAGTGGGAGAAATTCCTTGAGCCCTGGGAGTCAATG 62947
QY	421	CTCATTGAGCCATGATTCTGCCACTGCTGAGTGGGAGAAATTCCTTGAGCCCTGGGAGTCAATG 480
DB	62948	CTCATTGAGCCATGATTCTGCCACTGCTGAGTGGGAGAAATTCCTTGAGCCCTGGGAGTCAATG 63007
QY	481	AAAAAAGAAGTCTGACACTTTGCTACACATGGAATGAACTTGAATGTTATGCTAAA 540
DB	63008	AAAAAAGAAGTCTGACACTTTGCTACACATGGAATGAACTTGAATGTTATGCTAAA 63067
QY	541	GAATATGAGCTACCAAAAGACAAATCTCTATGAGTCCACTTTACATGAGTACTTTAG 600
DB	63068	GAATATGAGCTACCAAAAGACAAATCTCTATGAGTCCACTTTACATGAGTACTTTAG 63127
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QY	661	GGAATGGAAGTGAATGGGTATAGAGTTTATGTTTGAAGCTGAAAAGTCTCTGA 720
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QY	721	GATTGCTTAAACATATGAATGACTTACACTACAGACTATAGAAAGTCTTAAAAG 780
DB	63248	GATTGCTTAAACATATGAATGACTTACACTACAGACTATAGAAAGTCTTAAAAG 63306
QY	781	GCAATTTTATATTTATGTTATTTTACCACAAATTCGAAATTTTAAAATTTTCTCTCTG 840
DB	63307	GCAATTTTATATTTATGTTATTTTACCACAAATTCGAAATTTTAAAATTTTCTCTCTG 63366
QY	841	TTATTGACAGATATTGCTGTATATAAAGTTTTAAATTTGGCTGGCGAGTGGCTCA 900
DB	63367	TTATTGACAGATATTGCTGTATATAAAGTTTTAAATTTGGCTGGCGAGTGGCTCA 63426
QY	901	TACCTATATCCACTACTTTGGGAGCCAGGCAAGCAGATGCTGTAATCCAGAAATT 960
DB	63427	TACCTATATCCACTACTTTGGGAGCCAGGCAAGCAGATGCTGTAATCCAGAAATT 63486





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Db	69028	CAAGGGTGACACCAAGATTTATTCCTCCGGGGAGCTGAAGCATTAAGAACTAAGTGTGT	689688
Qy	4539	TTTGATTTACAGAGAGCTCTGAGCCTTAGTCTTCTGTGATGTGGGGGTCAAGATTGTT	4598
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Qy	4599	AGGCTGTAAAGATGCCACTTTATTAATTAACCTTCTACACCAACCATCTAGTTGTCTC	4658
Db	68808	AGGCTGTAAAGATGCCACTTTATTAATTAACCTTCTACACCAACCATCTAGTTGTCTC	688449
Qy	4659	TTAAAGCTGTGTCTCAATATGCAAAATGAATAGTTTGAACTTCACAGAGATTTCTTA	4718
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Qy	4839	TTCCCTCAACTGTAAATGAAGAAATTAATAGTACCATTTCCTATGATTAATGTGTAATG	4898
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QY	5729	CACTTTGGGAGGCGAGGAGCGGTGATCACAGTCAGAGGTTTCAGAGCCAGCTGAA	5798
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Db	67588	AGGTTGCAGTGAGCAGAGATCATGCCATTCAGCTCCAGCCTGGGCGACAGAGGAGACTC	67522
QY	5979	CATCTCAAAAAAAGCAAAACAGTTACAACTCATATTTGTCGAGTTTCAGA	6038
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Db	67469	TGGCAATGCGCAACCAAACTATACAGCCTATGTGAAGACCTAGTTGTAAGCTTTTC	67411
QY	6099	GTTAATGATGGGAAAAAGTTTACATCTTATATATGTAATGATAGGGTTTATTTTTGT	6158
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QY	6159	CTGTCCAAGCACCCCTCTCTGTGAGAGCTGCCGAATGCTGATTACCTTCCTTTGGTT	6218
Db	67349	CTGTCCAAGCACCCCTCTCTGTGAGAGCTGCCGAATGCTGATTACCTTCCTTTGGTT	67296
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Db	67169	TCGGGACATGGTAGAGATTCACTTACTCTGACCTTATTTATGAGACTGTCCTTAGCTT	67111
QY	6399	GTCATGATAGTTTCAAAATCTTAGCTGTATGATAGTATTTCACAAATCTTAGCAACATAT	6458
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+QY	6459	TGCATATCTTTTAATCCTTGAGCTATCTTTGGTTTGAGAAAGGCTATACCATAGACA	6518
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\* 101710 101809: gap of 100 bp  
 \* 101810 107002: contig of 5193 bp in length  
 \* 107003 107102: gap of 100 bp  
 \* 107103 111862: contig of 4760 bp in length.

## FEATURES

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Query Match 16.0%; Score 4624; DB 2; Length 111862;  
 Best Local Similarity 99.7%; Prod. No. 0;  
 Matches 5934; Conservative 0; Mismatches 7; Indels 9; Gaps 7;

QY 3159 ATTTATTTTAGGATATTTAAAGAAATACAAACTGGGTGCGAGTGGCCCGCCCTATATCT 3218  
 DB 70348 ATTTATTTTAGGATATTTAAAGAAATACAAACTGGGTGCGAGTGGCCCGCCCTATATCT 70289

QY 3219 CAGCACTTTGGGAAGCTGAGGGGGTGGATCACCTCAGGTGAGGTTCGAGACCAAGCCT 3278  
 DB 70288 CAGCACTTTGGGAAGCTGAGGGGGTGGATCACCTCAGGTGAGGTTCGAGACCAAGCCT 70229

QY 3279 GCCCAACATGGCGAGACCCGCTCTCTACTAAAAATACAAAATTTAGCCAAAGCGTGAGGCC 3338  
 DB 70228 GCCCAACATGGCGAGACCCGCTCTCTACTAAAAATACAAAATTTAGCCAAAGCGTGAGGCC 70169

QY 3339 AGTGCCTGTAAATCCCAAGCTACTCAGGAGGCAAGCTGGAGAAATCGCTTGAACCCGGAGGT 3398

DB 70168 AGTGCCTGTAAATCCCAAGCTACTCAGGAGGCAAGCTGGAGAAATCGCTTGAACCCGGAGGT 70109  
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 QY 3759 ACATCATATGATCCCTATTTAGATTTATATGATGATTTGGAATTCACATATAGG 3818  
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RESULT 2  
 AL139143/c  
 LOCUS  
 DEFINITION Homo sapiens chromosome 1, clone RP4-535P23 map p34.1-34.3, \*\*\*  
 SEQUENCING IN PROGRESS \*\*\*  
 ACCESSION AL139143  
 VERSION AL139143.6 GI:9863524  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_CANCELLED.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS Plumb, B.  
 TITLE Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 REQUESTS: clones@hinxton.sanger.ac.uk  
 On Aug 21, 2000 this sequence version replaced gi:9212183.  
 JOURNAL  
 COMMENT  
 Center: Sanger Centre  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
 Project Information  
 Center project name: dJ555P23  
 Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Sequencing vector: plasmid; L08752; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Consensus quality: 105509 bases at least Q40  
 Consensus quality: 107835 bases at least Q30  
 Consensus quality: 109154 bases at least Q20  
 Insert size: 110362; sum-of-ctrls  
 Insert size: 138096; 6.8% error; agarose-fp  
 Quality coverage: 3.57x in Q20 bases; sum-of-ctrls Quality  
 coverage: 3.11x in Q20 bases; agarose-fp  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 16 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 6110: contig of 6110 bp in length  
 \* 6111 6210: gap of 100 bp  
 \* 6211 12365: contig of 6155 bp in length  
 \* 12366 12465: gap of 100 bp  
 \* 12466 14908: contig of 2443 bp in length  
 \* 14909 15008: gap of 100 bp  
 \* 15009 17724: contig of 2716 bp in length  
 \* 17725 17824: gap of 100 bp  
 \* 17825 25035: contig of 7211 bp in length  
 \* 25036 25135: gap of 100 bp  
 \* 25136 27936: contig of 2801 bp in length  
 \* 27937 28036: gap of 100 bp  
 \* 28037 31938: contig of 3902 bp in length  
 \* 31939 32038: gap of 100 bp  
 \* 32039 44844: contig of 12806 bp in length  
 \* 44845 44944: gap of 100 bp  
 \* 44945 57247: contig of 12303 bp in length  
 \* 57248 57347: gap of 100 bp  
 \* 57348 63813: contig of 6466 bp in length  
 \* 63814 63913: gap of 100 bp  
 \* 63914 70362: contig of 6449 bp in length  
 \* 70363 70462: gap of 100 bp  
 \* 70463 80246: contig of 9784 bp in length  
 \* 80247 80346: gap of 100 bp  
 \* 80347 94000: contig of 13654 bp in length  
 \* 94001 94100: gap of 100 bp  
 \* 94101 101709: contig of 7609 bp in length



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Qy	21601	AGCCACAGATACCCCTTCACTTGGGGGTGAATTTATTTCTCTGCTCTGCTCTGCTCTG	21660
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Qy	21781	ACCAGGACTGCTGTGTGACCACTGACTGTATTAATATACAGTGTGATTAATTTCCATAC	21840
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Qy	22981	TGCTCCTTTTGGCCAGAAATGCAATAACAAGAGAGCTAGCGGTGGTGGGCACTTATAT	23040
Db	92428	TGCTCCTTTTGGCCAGAAATGCAATAACAAGAGAGCTAGCGGTGGTGGGCACTTATAT	92487
Qy	23041	GATTTACCTAAGGACTAAGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	23100
Db	92488	GATTTACCTAAGGACTAAGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	92547
Qy	23101	GAAGGTGATAGCTCGGCGGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT	23160
Db	92548	GAAGGTGATAGCTCGGCGGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT	92607
Qy	23161	GTCAGGCGGCGAGATCAATTTGAGGCTCAGGAAATTTGAAATCAGCTGACCAACATGGTGA	23220
Db	92608	GTCAGGCGGCGAGATCAATTTGAGGCTCAGGAAATTTGAAATCAGCTGACCAACATGGTGA	92667
Qy	23221	AACCTGTCTCTACTTAAATACAAAAATTTAGCCGGGTGGTGGCAGCCCTGTAAACC	23280
Db	92668	AACCTGTCTCTACTTAAATACAAAAATTTAGCCGGGTGGTGGCAGCCCTGTAAACC	92727
Qy	23281	CCAGCTACTCGGAGGCTGAGGAGGAGGAGTACTTGAACCTGGGAGGAGGTTGAG	23340
Db	92728	CCAGCTACTCGGAGGCTGAGGAGGAGGAGTACTTGAACCTGGGAGGAGGTTGAG	92787
Qy	23341	TGAGCTGAGATCGGCCCACTGCACTCCAGCTGGGTGACAGTGAACCTCTGCTCTGGGAA	23400
Db	92788	TGAGCTGAGATCGGCCCACTGCACTCCAGCTGGGTGACAGTGAACCTCTGCTCTGGGAA	92847

QY	19021	CCAGCTCTCCATTGAGCGCTGCTGAGACAGAGCGGTTTATATACACCAGCTCCCAATC	19080
Db	88468	CCAGCTCTCTCCATTGAGCGCTGCTGAGACAGAGCGGTTTATATACACCAGCTCCCAATC	88527
QY	19081	CTATTGAGCGCTCCCGCCGACAGACCAACGGCTCCAGCCCATTCAGCTGGCCCTT	19140
Db	88528	CTATTGAGCGCTCCCGCCGACAGACCAACGGCTCCAGCCCATTCAGCTGGCCCTT	88587
QY	19141	TGTCGTGGGGGTTAAGTGTGTACATGTGGGGGGCACCCAGAAAGAACTGTCAAGGCTTG	19200
Db	88588	TGTCGTGGGGGTTAAGTGTGTACATGTGGGGGGCACCCAGAAAGAACTGTCAAGGCTTG	88647
QY	19201	AAAGCGTGTGCTATACAGTGGCCCTCTACTGATGATGGGTGGGTGGAGACAGTGG	19260
Db	88648	AAAGCGTGTGCTATACAGTGGCCCTCTACTGATGATGGGTGGGTGGAGACAGTGG	88707
QY	19261	GGCGCCGGAAGGTGGGGGTGGGGAGAGAGCATGGGATTATGAGGCCACAGAGGACGT	19320
Db	88708	GGCGCCGGAAGGTGGGGGTGGGGAGAGAGCATGGGATTATGAGGCCACAGAGGACGT	88767
QY	19321	GCATAGAAAGGGGTGGMACAGGAGACCCCTCTCTCTTCTCTCTTCTACTTCACTTCTC	19380
Db	88768	GCATAGAAAGGGGTGGMACAGGAGACCCCTCTCTCTTCTCTCTTCTACTTCACTTCTC	88827
QY	19381	CGTCTAGCTTACTCCCTCTCTTGTGGGCACATGATGATCAAGAGCCCTTGGACCTTGAT	19440
Db	88828	CGTCTAGCTTACTCCCTCTCTTGTGGGCACATGATGATCAAGAGCCCTTGGACCTTGAT	88887
QY	19441	TTGGCTTTCTGATGCTCGGTGACACCGCTTGATGCTGACCTGAGAGAAATTTATATTA	19500
Db	88888	TTGGCTTTCTGATGCTCGGTGACACCGCTTGATGCTGACCTGAGAGAAATTTATATTA	88947
QY	19501	CGTTTCATTTCTTCCACAGACTCCGAAAGACGTGTTCCTCTCTTCCCTTCCCTGGAAAGGGT	19560
Db	88948	CGTTTCATTTCTTCCACAGACTCCGAAAGACGTGTTCCTCTCTTCCCTTCCCTGGAAAGGGT	89007
QY	19561	GGGTGGAAGGGGAACAGTGTGTGGGACAGAGGGAGATTCATTTCCTACGTTTCATTCG	19620
Db	89008	GGGTGGAAGGGGAACAGTGTGTGGGACAGAGGGAGATTCATTTCCTACGTTTCATTCG	89067
QY	19621	TGCAGTGAATTTGCAGCTGTGCCCTCCGCAACTTTTAAAGCTTCTCTGAAGTTCCCTCG	19680
Db	89068	TGCAGTGAATTTGCAGCTGTGCCCTCCGCAACTTTTAAAGCTTCTCTGAAGTTCCCTCG	89127
QY	19681	GAGCCCTTAGGTGGAGGGGTTTAGGGGAACACAGATCTCAACTGATATATTGGAAAGAT	19740
Db	89128	GAGCCCTTAGGTGGAGGGGTTTAGGGGAACACAGATCTCAACTGATATATTGGAAAGAT	89187
QY	19741	TTTGTGAGGAAAGAAATTAATCTTCAAGGCTCTTAAATTCGTTTAAACTCTTATATGCA	19800
Db	89188	TTTGTGAGGAAAGAAATTAATCTTCAAGGCTCTTAAATTCGTTTAAACTCTTATATGCA	89247
QY	19801	ATGTACCCCTTGTGATTTTACAGCTGGGAAAAACGCAAAAATGGAAGATAGGGGAATGC	19860
Db	89248	ATGTACCCCTTGTGATTTTACAGCTGGGAAAAACGCAAAAATGGAAGATAGGGGAATGC	89307
QY	19861	GCATTTTACCTAAGTGAACATAGTAATTTCTGTAGACTTAAAGAGCACTTTAC	19920
Db	89308	GCATTTTACCTAAGTGAACATAGTAATTTCTGTAGACTTAAAGAGCACTTTAC	89367
QY	19921	CTTTAAGACAGATGAGAAATGATGAACAAACAGTAGTCAATCAGCTTCTCTAGGCC	19980
Db	89368	CTTTAAGACAGATGAGAAATGATGAACAAACAGTAGTCAATCAGCTTCTCTAGGCC	89427
QY	19981	TTCTCTTCCCAAGATGAACCAATCTGTGGGAATATTTGTCGTTCCATTTGCTTTAATGG	20040
Db	89428	TTCTCTTCCCAAGATGAACCAATCTGTGGGAATATTTGTCGTTCCATTTGCTTTAATGG	89487
QY	20041	CTCTTTGGCATGTCAAAGCTCCTCTGGGGTGTGTGCTGCTGTCTGGAGCCCAAGTACAA	20100
Db	89488	CTCTTTGGCATGTCAAAGCTCCTCTGGGGTGTGTGCTGCTGTCTGGAGCCCAAGTACAA	89547
QY	20101	TGTTCCACCACATATCTTATTGAACAATTTTAAAGCATATATATTATTATAGCCCAAAAAG	20160

Db	89548	TGTGACCACTATGTTATTGAAACAATTTTAAAGCATATATATTTTATTTATTTAGCCCAAAAG	89607
QY	20161	GTTAAATGATTTGATTTTGCCCTAACTTCCCAAGACATGTGGGAGTGCAGATGATG	20226
Db	89608	GTTAAATGATTTGATTTTGCCCTAACTTCCCAAGACATGTGGGAGTGCAGATGATG	89666
QY	20221	TGACCTCAGAGAGAGAGAAAGAGAGGTTAGCAACGATGTTTAAATCCAGATGCTGC	20286
Db	89668	TGACCTCAGAGAGAGAGAGAAAGAGAGGTTAGCAACGATGTTTAAATCCAGATGCTGC	89722
QY	20281	TTTGTTCGTATATGGAACCTCTGAGGGCTTCTAGTACTTCTGCTGCTGCTGCCAGGAT	20341
Db	89728	TTTGTTCGTATATGGAACCTCTGAGGGCTTCTAGTACTTCTGCTGCTGCTGCCAGGAT	89788
QY	20341	GGAGGCCAAGGCTCTGGGATGTGTCAAGAACTTTACAACGTGGGCAACTTTATCTTC	20400
Db	89788	GGAGGCCAAGGCTCTGGGATGTGTCAAGAACTTTACAACGTGGGCAACTTTATCTTC	89844
QY	20401	TAGCCCTACCTTACCTCCATTTCCACGAGCTCCACGACACTGGCTACGGGGGTGTT	20466
Db	89848	TAGCCCTACCTTACCTCCATTTCCACGAGCTCCACGACACTGGCTACGGGGGTGTT	89907
QY	20461	CCTGAACCTACTGTGAAAAATGCAGTCTCTATATGCTTCTGTGCTTCTCTGGTAGCT	20526
Db	89908	CCTGAACCTACTGTGAAAAATGCAGTCTCTCTATATGCTTCTGTGCTTCTCTGGTAGCT	89966
QY	20521	CTTATATCTCCTCAAGGCTCTGGCTCAAAATATCACCTCTGTGCTAGTGGGTTATGGC	20586
Db	89966	CTTATATCTCCTCAAGGCTCTGGCTCAAAATATCACCTCTGTGCTAGTGGGTTATGGC	90027
QY	20581	TCATGCGCTATATCCAGAAATGTTGGAGGCCAAGCTGGAGAGTCACTTAAAGTTGGGA	20640
Db	90028	TCATGCGCTATATCCAGAAATGTTGGAGGCCAAGCTGGAGAGTCACTTAAAGTTGGGA	90088
QY	20641	GTTGAGAGCAGGCGGGTAACTAGGAAGAGTCCCATCTCTTAAAAATAAAAAATCAC	20700
Db	90088	GTTGAGAGCAGGCGGGTAACTAGGAAGAGTCCCATCTCTTAAAAATAAAAAATCAC	90147
QY	20701	CTGTGTGAAGCTTTCCTTACCTTTTCTGGGCTTACTACTTGTGCTGCTGCTCTGTAT	20766
Db	90148	CTGTGTGAAGCTTTCCTTACCTTTTCTGGGCTTACTACTTGTGCTGCTGCTCTGTAT	90207
QY	20761	GCAGGGCCCATATGATTGTTATAGCCCAACCTTCTGTATTCCTTTTCTTTGAGACAGG	20820
Db	90208	GCAGGGCCCATATGATTGTTATAGCCCAACCTTCTGTATTCCTTTTCTTTGAGACAGG	90267
QY	20821	GTCGTGGCTGTGTCACCCAGGCTAGAGAGTCCGTGGTGATCTTGGGTCACCTGCACCTGT	20886
Db	90268	GTCGTGGCTGTGTCACCCAGGCTAGAGAGTCCGTGGTGATCTTGGGTCACCTGCACCTGT	90327
QY	20881	GCCTCCCAAGTTCAAGCAGTTCTGTGCTCCAGCTTCCCAAGTAGTGGTGGATTACAGGGC	20940
Db	90328	GCCTCCCAAGTTCAAGCAGTTCTGTGCTCCAGCTTCCCAAGTAGTGGTGGATTACAGGGC	90387
QY	20941	TGTCCACCAATGCCCCGCTAATTTTGTATTTTACTAAGAGAGGGGTTTCAACATGTTG	21000
Db	90388	TGTCCACCAATGCCCCGCTAATTTTGTATTTTACTAAGAGAGGGGTTTCAACATGTTG	90447
QY	21001	ATCAGGCTGTCTTAAACCTCCTAGGCTCCAGTAGTCTGTCCGCTTGCCCTCCCAAGTG	21060
Db	90448	ATCAGGCTGTCTTAAACCTCCTAGGCTCCAGTAGTCTGTCCGCTTGCCCTCCCAAGTG	90507
QY	21061	CTGGAATTTAAGGCATGAGCAACACACATGACTTCTGTTCCCTTCTTAAACAAGAG	21120
Db	90508	CTGGAATTTAAGGCATGAGCAACACACATGACTTCTGTTCCCTTCTTAAACAAGAG	90567
QY	21121	CTCCCCAAGCACAGCAAGTCTGATTTGTGCTGCTGAATTTCCCAACAGTACCTGGGAC	21180
Db	90568	CTCCCCAAGCACAGCAAGTCTGATTTGTGCTGCTGAATTTCCCAACAGTACCTGGGAC	90627
QY	21181	AAAGTAGACCTGTATCTGTATGCTATACATGTTAAATGAATGGTGGGAAGGACACAGT	21240

Db	86248	TTGGCTGCCATAGAGGAATGTTCTGGCTGAAGCAGAAAGCAAGCAATCCAGTTCATAC	86307
QY	16861	ACATATGACACACAGAGACAGCAGCCCTTTCTGGCTGAGAAATCTTTGGCGG	16920
Db	86308	ACATATGACACACAGAGACAGCAGCCCTTTCTGGCTGAGAAATCTTTGGCGG	86367
QY	16921	CAGCAATAGCACTTGTCCCATGTTGAGTGGCATTTTTTCAAGTGTCAATGGACTGTGA	16980
Db	86368	CAGCAATAGCACTTGTCCCATGTTGAGTGGCATTTTTTCAAGTGTCAATGGACTGTGA	86427
QY	16981	AAGCTACTTAATAAATTTGATCTCATCTCAATAATCTGAGTTAATAGCTTCAAGCTTG	17040
Db	86428	AAGCTACTTAATAAATTTGATCTCATCTCAATAATCTGAGTTAATAGCTTCAAGCTTG	86487
QY	17041	TGAGGATTAATAAATAAATAATTTGAAGTGTCTGCTCAAGGCTTGGCAGAGTAAT	17100
Db	86488	TGAGGATTAATAAATAAATAATTTGAAGTGTCTGCTCAAGGCTTGGCAGAGTAAT	86547
QY	17101	CTCAACAAATGCTGTTGAATGAATGAATCCATGAATCTGAGCAATTAAGGCCCTCCAC	17160
Db	86548	CTCAACAAATGCTGTTGAATGAATGAATCCATGAATCTGAGCAATTAAGGCCCTCCAC	86607
QY	17161	CGTTTCCAAGGATCAGTGCAATAACAGCCCGGTAACTGAGACTTGTAGACTGTCCCACT	17220
Db	86608	CGTTTCCAAGGATCAGTGCAATAACAGCCCGGTAACTGAGACTTGTAGACTGTCCCACT	86667
QY	17221	GAGCTCGAGCTGAGGCATGATCTAAACCTGCTTCCCTTTGACAAATATTTGATGAGT	17280
Db	86668	GAGCTCGAGCTGAGGCATGATCTAAACCTGCTTCCCTTTGACAAATATTTGATGAGT	86727
QY	17281	TATGGTGTGGAGGTGGACCTTCCATGAAGGCTTCTTGCCCTAGCTGTTGGAAGCACT	17340
Db	86728	TATGGTGTGGAGGTGGACCTTCCATGAAGGCTTCTTGCCCTAGCTGTTGGAAGCACT	86787
QY	17341	ATCGACAGACTTTCAGAGGTGGGAATTCCTCAGAGAGCACCTTGCCCAAGGTCAAGGA	17400
Db	86788	ATCGACAGACTTTCAGAGGTGGGAATTCCTCAGAGAGCACCTTGCCCAAGGTCAAGGA	86847
QY	17401	TAGCCCAATTCATATGCAACAGCTGTGAACGCTTCCCTGAGAGTTCAGTATTTGGGT	17460
Db	86848	TAGCCCAATTCATATGCAACAGCTGTGAACGCTTCCCTGAGAGTTCAGTATTTGGGT	86907
QY	17461	CAACTCTGAAGGCCATTCAGAGTTCAGAGTCCCTGAGAGTTCAGAGTTCAGTATTTGGGT	17520
Db	86908	CAACTCTGAAGGCCATTCAGAGTTCAGAGTCCCTGAGAGTTCAGAGTTCAGTATTTGGGT	86967
QY	17521	GGCTGTGCTTGTAGATCAGCTCTTCTCTGGCCACTCTGCTCATCTCTCATTTCCAC	17580
Db	86968	GGCTGTGCTTGTAGATCAGCTCTTCTCTGGCCACTCTGCTCATCTCTCATTTCCAC	87027
QY	17581	AGCTGTGTATCCCAAGGAGGTTCCTTAATAACATCCAGCACATTAACAGTCTCAGAGT	17640
Db	87028	AGCTGTGTATCCCAAGGAGGTTCCTTAATAACATCCAGCACATTAACAGTCTCAGAGT	87087
QY	17641	TGCTTCTGGGAAATCCAGCTATGAATGCACTAGTCTGCTGGCCAGAGCTTTAGAAC	17700
Db	87088	TGCTTCTGGGAAATCCAGCTATGAATGCACTAGTCTGCTGGCCAGAGCTTTAGAAC	87147
QY	17701	AACAAAGACGGAGACTCTTCTGCAATGGATTTCCAGCTTGGAGGTGTGGATGTCT	17760
Db	87148	AACAAAGACGGAGACTCTTCTGCAATGGATTTCCAGCTTGGAGGTGTGGATGTCT	87207
QY	17761	CTTTATGCCACACAGGCGCAGCAGCATCTAGCCACCTTCCCTTCTGAGGCTCCAGGAG	17820
Db	87208	CTTTATGCCACACAGGCGCAGCAGCATCTAGCCACCTTCCCTTCTGAGGCTCCAGGAG	87267
QY	17821	TGGGCTTGAAGCCCTTTTCCCGGCAACTTACGCCCCACACAGGATTTGGCAGGATCAC	17880
Db	87268	TGGGCTTGAAGCCCTTTTCCCGGCAACTTACGCCCCACACAGGATTTGGCAGGATCAC	87327
QY	17881	CTCCCTTAGGGTCTTACCCCTCTGACTATAACACAAACATTTCTTAACTGTCCAGGC	17940
Db	87328	CTCCCTTAGGGTCTTACCCCTCTGACTATAACACAAACATTTCTTAACTGTCCAGGC	87387
QY	17941	CTTAGTTTTGTAGTCTCAAGCTCCTGTACCACCATCAGTGAAGGCCAATCAGTCTTCCT	18000
Db	87388	CTTAGTTTTGTAGTCTCAAGCTCCTGTACCACCATCAGTGAAGGCCAATCAGTCTTCCT	87447
QY	18001	ACTGTGCCCTTCCCTTGCCTCCTGTCGGCAAGCTCCGTCCTGGGATCCCCACCTCT	18060
Db	87448	ACTGTGCCCTTCCCTTGCCTCCTGTCGGCAAGCTCCGTCCTGGGATCCCCACCTCT	87507
QY	18061	CACACTTACCACCCACAATAAGATTTGTTTCTGTGTCACAAGGTAATTAACAAGCTTGGG	18120
Db	87508	CACACTTACCACCCACAATAAGATTTGTTTCTGTGTCACAAGGTAATTAACAAGCTTGGG	87567
QY	18121	CCAGTAGGCCAGGGCCAGTCTGAGGATGTCATCTATCTGGCTCTCCCTGTTCTGC	18180
Db	87568	CCAGTAGGCCAGGGCCAGTCTGAGGATGTCATCTATCTGGCTCTCCCTGTTCTGC	87627
QY	18181	TAAAGGTATTTTCAAGTTTATTTATATGATGATGTGTGTGATCTGGCCCTG	18240
Db	87628	TAAAGGTATTTTCAAGTTTATTTATATGATGATGTGTGTGATCTGGCCCTG	87687
QY	18241	GTGACATGACATATGGAGCAAGAGCGGAGAGCAAAATTTCCCTTTGTCACAAATTTGACT	18300
Db	87688	GTGACATGACATATGGAGCAAGAGCGGAGAGCAAAATTTCCCTTTGTCACAAATTTGACT	87747
QY	18301	TCTTGAACCGCACCCACACACACACACACACACACACACACACACACACACACAC	18360
Db	87748	TCTTGAACCGCACCCACACACACACACACACACACACACACACACACACACACAC	87807
QY	18361	TTTGCTTACCTGTCTTCAATTTCTGTCCTCATCCCCAAGATTTCTAAGAGATTTCTCTG	18420
Db	87808	TTTGCTTACCTGTCTTCAATTTCTGTCCTCATCCCCAAGATTTCTAAGAGATTTCTCTG	87867
QY	18421	GGAATTTGGAGCCAGATGGATGTCATACAGAGAGGAGGAAAGGCTTGGGAAGAGAGTG	18480
Db	87868	GGAATTTGGAGCCAGATGGATGTCATACAGAGAGGAGGAAAGGCTTGGGAAGAGAGTG	87927
QY	18481	ACAGCAGCAAGCAATACCTTTTGTAGCAGCATTAACTCATCCAGCAAACTTTACT	18540
Db	87928	ACAGCAGCAAGCAATACCTTTTGTAGCAGCATTAACTCATCCAGCAAACTTTACT	87987
QY	18541	ACATTTCCCATCCTGTCTAGTCTTCTAGGCTTAAGCTTCCCAACTCCCTGCTGGGGCC	18600
Db	87988	ACATTTCCCATCCTGTCTAGTCTTCTAGGCTTAAGCTTCCCAACTCCCTGCTGGGGCC	88047
QY	18601	ATCCTGTGAGACAGTGTTCATGCTGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	18660
Db	88048	ATCCTGTGAGACAGTGTTCATGCTGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	88107
QY	18661	GTTCCTATGGGTGTGAGGAAACCTGGCCAGAAAGCTTTGAGAGAGTGAGATTGAGTT	18720
Db	88108	GTTCCTATGGGTGTGAGGAAACCTGGCCAGAAAGCTTTGAGAGAGTGAGATTGAGTT	88167
QY	18721	TGGGTCAACCACTCAAGAGAGGATGCTTGGCTGAATTTAAGGCTTACTTAAGGCTTCC	18780
Db	88168	TGGGTCAACCACTCAAGAGAGGATGCTTGGCTGAATTTAAGGCTTACTTAAGGCTTCC	88227
QY	18781	GTAAATGTAGTCTACTTCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	18840
Db	88228	GTAAATGTAGTCTACTTCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	88287
QY	18841	AGTGGAGGGGGGACTCTGAACTGCAATGATTCGCTGGGAAATCAGCTGAGGCTGAGGCG	18900
Db	88288	AGTGGAGGGGGGACTCTGAACTGCAATGATTCGCTGGGAAATCAGCTGAGGCTGAGGCG	88347
QY	18901	GATTTGTGGGCGCATTTTCCCGGCAACTTCTCTCTGCTGTGCTGCCAGAGAGTAATAA	18960
Db	88348	GATTTGTGGGCGCATTTTCCCGGCAACTTCTCTCTGCTGTGCTGCCAGAGAGTAATAA	88407
QY	18961	ATCATTTGTAGGGCGGAGTGCAGCTGCCGAGCTTCCCTTCCCTTCCCTTCCCTTCCCT	19020
Db	88408	ATCATTTGTAGGGCGGAGTGCAGCTGCCGAGCTTCCCTTCCCTTCCCTTCCCTTCCCT	88467



OY	14641	AGCATATCGTGTGTAAGAAATGATGCTTGGGCTAGACACATGCTGCACATATAA	14700
DB	84088	AGCATATCGTGTGTAAGAAATGATGCTTGGGCTAGACACATGCTGCACATATAA	84147
OY	14701	TAATTCATGAAATTTTGGACAAATGAGTGAATGGAGGCTGGAAGAGCTAATGATGAAA	14760
DB	84148	TAATTCATGAAATTTTGGACAAATGAGTGAATGGAGGCTGGAAGAGCTAATGATGAAA	84207
OY	14761	AGCATAGAGTGAATTTATATACAGAGAGCTTTCTAGTGACAGACAGAAATAGAGGTAG	14820
DB	84208	AGCATAGAGTGAATTTATATACAGAGAGCTTTCTAGTGACAGACAGAAATAGAGGTAG	84267
OY	14821	AGCTTATGCTGCTGCTTCTTGCAGCTTGTAGCATATGACATTTGGTGAAGTACGCT	14880
DB	84268	AGCTTATGCTGCTGCTTCTTGCAGCTTGTAGCATATGACATTTGGTGAAGTACGCT	84327
OY	14881	CTTTTTCCTCACTGGAATAATGGGCTCATGTGAATGACTGGTGGTTCAGTCAAGGCT	14940
DB	84328	CTTTTTCCTCACTGGAATAATGGGCTCATGTGAATGACTGGTGGTTCAGTCAAGGCT	84387
OY	14941	ATGGTAGAGTCAAGTGAATTAATGTGAAGTGAATGTACATATTTAAGAGGCTGCA	15000
DB	84388	ATGGTAGAGTCAAGTGAATTAATGTGAAGTGAATGTACATATTTAAGAGGCTGCA	84447
OY	15001	CTAATGACAGCTTAACCTACTGCTGAGATGGGTAGAGCTGAGTGGAGGAAGAACCA	15060
DB	84448	CTAATGACAGCTTAACCTACTGCTGAGATGGGTAGAGCTGAGTGGAGGAAGAACCA	84507
OY	15061	GCCCCAACAAAGCTCCATAGTCCACACATTTGCTGCTACATATGCTGAGACTTTGTTATA	15120
DB	84508	GCCCCAACAAAGCTCCATAGTCCACACATTTGCTGCTACATATGCTGAGACTTTGTTATA	84567
OY	15121	GCATAGAAATGAGAGGCTGTGTATGCTGAGTCCAGTGAAGTGGGAGATAGAGCT	15180
DB	84568	GCATAGAAATGAGAGGCTGTGTATGCTGAGTCCAGTGAAGTGGGAGATAGAGCT	84627
OY	15181	GGCTTGTGTAGGCTGTGTACCTCAGATTTTACCTTTTGAAGCAAGTGGCTGCTT	15240
DB	84628	GGCTTGTGTAGGCTGTGTACCTCAGATTTTACCTTTTGAAGCAAGTGGCTGCTT	84687
OY	15241	CTGTCGCCAGTAAATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	15300
DB	84688	CTGTCGCCAGTAAATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	84747
OY	15301	TTTGCTCCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	15360
DB	84748	TTTGCTCCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	84807
OY	15361	CCCTGTGTGTGATTCATATGGAAGGAGGAGTTTGAAGTACAGCTTAAGGCTGA	15420
DB	84808	CCCTGTGTGTGATTCATATGGAAGGAGGAGTTTGAAGTACAGCTTAAGGCTGA	84867
OY	15421	TTGGAAGAGTGGGGGAGACCTGAGTTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	15480
DB	84868	TTGGAAGAGTGGGGGAGACCTGAGTTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	84927
OY	15481	CCGCGGAATTTCTTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	15540
DB	84928	CCGCGGAATTTCTTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	84987
OY	15541	CAGCTGAGACATTTATGCTGAGTCAAGGGGTAGAAAGTCTGAGGAGGTTGGAGT	15600
DB	84988	CAGCTGAGACATTTATGCTGAGTCAAGGGGTAGAAAGTCTGAGGAGGTTGGAGT	85047
OY	15601	GAGCGGTGTTTGGGTTTGGGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	15660
DB	85048	GAGCGGTGTTTGGGTTTGGGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	85107
OY	15661	AAGGCTAGTCCCAACCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	15720
DB	85108	AAGGCTAGTCCCAACCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	85167
OY	15721	CAAAAAGACAGTTATTGCAAAAACAGATGACCTAGCCAAAAATCATCTGGTTC	15780

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DB	85168	CAAAAAGACAGTTATTGCAAAAACAGATGACCTAGCCAAAAATCATCTGGTTC	85227
OY	15781	AAAGTGAATAATAGTTCCTGGGGCCACACAGGAAAGGCTGTGTGTGTGTGTGTGT	15840
DB	85228	AAAGTGAATAATAGTTCCTGGGGCCACACAGGAAAGGCTGTGTGTGTGTGTGTGT	85287
OY	15841	TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	15900
DB	85288	TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	85347
OY	15901	GAGTGAATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	15960
DB	85348	GAGTGAATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	85407
OY	15961	CCTTCATTTTCTTCAAGTTTATGATGATTAATGAAATTAAGAAATTAATTAATCTTCA	16020
DB	85408	CCTTCATTTTCTTCAAGTTTATGATGATTAATGAAATTAAGAAATTAATTAATCTTCA	85467
OY	16021	TGTTGGTTGCTGATGCTTAAATGACCAAGGATTTAGAACCCATCAGGGCTATAGAGAA	16080
DB	85468	TGTTGGTTGCTGATGCTTAAATGACCAAGGATTTAGAACCCATCAGGGCTATAGAGAA	85527
OY	16081	CAGCAGTGAAGTTCCTATCTATCTTTCACAGCTCCTTACACAGTGGGCAAG	16140
DB	85528	CAGCAGTGAAGTTCCTATCTATCTTTCACAGCTCCTTACACAGTGGGCAAG	85587
OY	16141	TTAGTGAAGTGAAGGCTAGTGAAGTTCCTGAAACAGAACTGCTGCTTGTGCC	16200
DB	85588	TTAGTGAAGTGAAGGCTAGTGAAGTTCCTGAAACAGAACTGCTGCTTGTGCC	85647
OY	16201	TTCAATGTTATTTGTTCCAAAGTTCGACAAATATGAGGTTAGACATTTAGGCAAGAC	16260
DB	85648	TTCAATGTTATTTGTTCCAAAGTTCGACAAATATGAGGTTAGACATTTAGGCAAGAC	85707
OY	16261	TTATCATCACTTTCTGATGATCAATGCTTAAAGAACTAGAGATCCAGGCTGCT	16320
DB	85708	TTATCATCACTTTCTGATGATCAATGCTTAAAGAACTAGAGATCCAGGCTGCT	85767
OY	16321	CTCATTTGATATTCAGGAGGAGTGAAGGCTTTCTTTTGGCAATGCTGCTGCT	16380
DB	85768	CTCATTTGATATTCAGGAGGAGTGAAGGCTTTCTTTTGGCAATGCTGCTGCTGCT	85827
OY	16381	TCTGTAGCTACACAGGAAATTTTAAACTGTGTGTGTGTGTGTGTGTGTGTGTGT	16440
DB	85828	TCTGTAGCTACACAGGAAATTTTAAACTGTGTGTGTGTGTGTGTGTGTGTGTGT	85887
OY	16441	TGCTGTAAATCCAGCACTTTGGAGGTTGAGGTGGGGGTTTCTTGAACCTCAGGGGT	16500
DB	85888	TGCTGTAAATCCAGCACTTTGGAGGTTGAGGTGGGGGTTTCTTGAACCTCAGGGGT	85947
OY	16501	TGACACACGCTGGGCAAAATGCGCAAAACCCATCTTACAAAAAATACAAAAATAGCT	16560
DB	85948	TGACACACGCTGGGCAAAATGCGCAAAACCCATCTTACAAAAAATACAAAAATAGCT	86007
OY	16561	GTGCATGGTGGCAGTCCCTGCTGCTTCAACTTTGGAGAGCTGAGGTAGGAAATACCT	16620
DB	86008	GTGCATGGTGGCAGTCCCTGCTGCTTCAACTTTGGAGAGCTGAGGTAGGAAATACCT	86067
OY	16621	TGAGCTGTGAGTGTGTGCTCAATGAGCCAAACTCAGAGTTCATTCAGCTGGGT	16680
DB	86068	TGAGCTGTGAGTGTGTGCTCAATGAGCCAAACTCAGAGTTCATTCAGCTGGGT	86127
OY	16681	GACAGAGTGAAGTCCCTCAAAAGAAAAAAGTGTGTGTGTGTGTGTGTGTGTGTGT	16740
DB	86128	GACAGAGTGAAGTCCCTCAAAAGAAAAAAGTGTGTGTGTGTGTGTGTGTGTGTGT	86187
OY	16741	ACCTTGAAGCAGCAATTTTGAAGGAAATTAAGCAGAGGCTATTTAGAGCATACCTC	16800
DB	86188	ACCTTGAAGCAGCAATTTTGAAGGAAATTAAGCAGAGGCTATTTAGAGCATACCTC	86247
OY	16801	TTGGCTGCATAGAGAAATGCTTGTGCTGAAGCAGAAACCATCCAGTTCATAC	16860

Db	81868	GCTCAGGCTGGGAGACTTTTTAGGGGGTGTTTTTTGGTTTTTATCTCCTCCTAGGGTTATGCT	81927
Qy	12481	AATCACTCTTGCGGATCCTGTGCTGGGATTTGGCTCCTTAAGGATACAGAGAGTATTT	12540
Db	81928	AATCACTCTTGCGGATCCTGTGCTGGGATTTGGCTCCTTAAGGATACAGAGAGTATTT	81987
Qy	12541	CTGGGAGAGTGTTCCTCCATGATATTTGATTTATGTCATCCTTTGAGATGATTTGATC	12600
Db	81988	CTGGGAGAGTGTTCCTCCATGATATTTGATTTATGTCATCCTTTGAGATGATTTGATC	82047
Qy	12601	TTCTACCTCTTATCTCTACTCATCGCTGGGCACACAGCTTGAATGTAGTGGCTCCTACC	12660
Db	82048	TTCTACCTCTTATCTCTACTCATCGCTGGGCACACAGCTTGAATGTAGTGGCTCCTACC	82107
Qy	12661	ACAGTTGGAATAAATAACACTACACCTTTTCAGAGCCTCTGTGTTATAAAATGAGGATAC	12720
Db	82108	ACAGTTGGAATAAATAACACTACACCTTTTCAGAGCCTCTGTGTTATAAAATGAGGATAC	82167
Qy	12721	AGTCATGCTGCTCTCAGAGTTGCTGGGGGCTTCAGTTGGAAATGTATGTCAGTGCATT	12780
Db	82168	AGTCATGCTGCTCTCAGAGTTGCTGGGGGCTTCAGTTGGAAATGTATGTCAGTGCATT	82227
Qy	12781	ATGTCAGTGGCCACTCTGTGAAGCATAAGAAATGGCCAGTAGCTCCCAAGAAAAAGAAAT	12840
Db	82228	ATGTCAGTGGCCACTCTGTGAAGCATAAGAAATGGCCAGTAGCTCCCAAGAAAAAGAAAT	82287
Qy	12841	CACCTCCTTTGAGAAATGAAGAAATACCAGTATCACAATTTATCATATATTTGTAGGCC	12900
Db	82288	CACCTCCTTTGAGAAATGAAGAAATACCAGTATCACAATTTATCATATATTTGTAGGCC	82347
Qy	12901	ACTTCTGAAAGGCCACTTGTTCCTCAAAATATCTCAAACTTTAAATGAAATGATGCTTC	12960
Db	82348	ACTTCTGAAAGGCCACTTGTTCCTCAAAATATCTCAAACTTTAAATGAAATGATGCTTC	82407
Qy	12961	TCTAAAAACCTGCTTCTCCTCTATTTTCCGATTTTCAGTAAAGGTACTCCTCATATATC	13020
Db	82408	TCTAAAAACCTGCTTCTCCTCTATTTTCCGATTTTCAGTAAAGGTACTCCTCATATATC	82467
Qy	13021	CAGTCACCTCAGACTGGAAATCTGGAGGACATCTTGACCTGTCTTTTAATCCTGTAATCA	13080
Db	82468	CAGTCACCTCAGACTGGAAATCTGGAGGACATCTTGACCTGTCTTTAATCCTGTAATCA	82527
Qy	13081	GACAAATTCGAAGTCTGTATTTCTACTTCCAAATTTGCATCTGGAATCAGTCAATTTCT	13140
Db	82528	GACAAATTCGAAGTCTGTATTTCTACTTCCAAATTTGCATCTGGAATCAGTCAATTTCT	82587
Qy	13141	TCCAGCTCTATGCCAGCCCCCTGGTCCAAAGATTTCCACAAATTTCTTCTAGGCTCCTACC	13200
Db	82588	TCCAGCTCTATGCCAGCCCCCTGGTCCAAAGATTTCCACAAATTTCTTCTAGGCTCCTACC	82647
Qy	13201	GTAGCCTCTGACCCCCCACTTCTGTTTTGCTTTTTCATCCAAATCTGCACAGCAG	13260
Db	82648	GTAGCCTCTGACCCCCCACTTCTGTTTTGCTTTTTCATCCAAATCTGCACAGCAG	82707
Qy	13261	CCAGAGCGGACCTTTATGTAAATATAAATTTGGAGGATGACCTTCACTACTTAAATCTT	13320
Db	82708	CCAGAGCGGACCTTTATGTAAATATAAATTTGGAGGATGACCTTCACTACTTAAATCTT	82767
Qy	13321	TTAATGCTTCCGCTGCACCTCAAGTTTCAAACTTCTCATGCGCGATGCATGACATAGCTC	13380
Db	82768	TTAATGCTTCCGCTGCACCTCAAGTTTCAAACTTCTCATGCGCGATGCATGACATAGCTC	82827
Qy	13381	TGCTCCCAACCTGCTGCTACTTCTTCTTCATGAGATGACCTTCCATCCCTCTCTTTGCTGACTAA	13440
Db	82828	TGCTCCCAACCTGCTGCTACTTCTTCTTCATGAGATGACCTTCCATCCCTCTCTTTGCTGACTAA	82887
Qy	13441	AGTGTCTCTTTCCCTGGAAATGCCCTCCCTACATCCATCCTCTCTCTTTGCTGACTAA	13500
Db	82888	AGTGTCTCTTTCCCTGGAAATGCCCTCCCTACATCCATCCTCTCTCTTTGCTGACTAA	82947
Qy	13501	TGCATAATTTCTCAAGTGTATAGCTTAAGCCTTAATTTCTCAGAGAGCCCTTCTCTGACCA	13560
Db	82948	TGCATAATTTCTCAAGTGTATAGCTTAAGCCTTAATTTCTCAGAGAGCCCTTCTCTGACCA	83007
Qy	13561	TTAACACCCCTTCTTTTTTCTTTTCTTTTCTTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGTCTCGGCC	13620
Db	83008	TTAACACCCCTTCTTTTTTCTTTTCTTTTCTTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGTCTCGGCC	83067
Qy	13621	TGTCGCCCAGGCTGGAATCCAGTGTGACGATCTCGGCTCACTGCAACCTCTGCCCTCCCGG	13680
Db	83068	TGTCGCCCAGGCTGGAATCCAGTGTGACGATCTCGGCTCACTGCAACCTCTGCCCTCCCGG	83127
Qy	13681	GTTCAGCGCATTTCTCCTCGCCCAGGCTCCCAAGTAGCTGGGATACAGGATGCGGCCACT	13740
Db	83128	GTTCAGCGCATTTCTCCTCGCCCAGGCTCCCAAGTAGCTGGGATACAGGATGCGGCCACT	83187
Qy	13741	ACACCCAGCTAAATTTTGTATTTTTCAGTAGAGACGGGTTTCACTATGTTGGTCAAGGCTG	13800
Db	83188	ACACCCAGCTAAATTTTGTATTTTTCAGTAGAGACGGGTTTCACTATGTTGGTCAAGGCTG	83247
Qy	13801	GTCTCGAACTCTTGACCTCGTGATCCGCCCGCTTGGCTCCACAGTGTGGGATACACA	13860
Db	83248	GTCTCGAACTCTTGACCTCGTGATCCGCCCGCTTGGCTCCACAGTGTGGGATACACA	83307
Qy	13861	GGCATGAGCCACCAAGTCCAGCTTAACACCCCTTTCTTAATTTAGTTTACCTTTCTATTAAG	13920
Db	83308	GGCATGAGCCACCAAGTCCAGCTTAACACCCCTTTCTTAATTTAGTTTACCTTTCTATTAAG	83367
Qy	13921	TTTCTCTATTTCTTTTTTTTGAGATGGATTCTCGCTGTGTCGCCCGGCTGGAGTGAGTGC	13980
Db	83368	TTTCTCTATTTCTTTTTTTTGAGATGGATTCTCGCTGTGTCGCCCGGCTGGAGTGAGTGC	83427
Qy	13981	AGTAGCAGATCTCAGCTCACTGCAACCTTTGTCTCCCCCTTCAAGCAATCTCTGCTCA	14040
Db	83428	AGTAGCAGATCTCAGCTCACTGCAACCTTTGTCTCCCCCTTCAAGCAATCTCTGCTCA	83487
Qy	14041	GCCTCCCAAGGGCTGGGTTTACAGGACGCCACACACACCCCGCTTAATTTTGTATTT	14100
Db	83488	GCCTCCCAAGGGCTGGGTTTACAGGACGCCACACACACCCCGCTTAATTTTGTATTT	83547
Qy	14101	TTGATAGAGCGGGGAAGGTGTAGCTTAAGCCTTAACCTTCTTACAGAGAAGCCTTCTCTGA	14160
Db	83548	TTGATAGAGCGGGGAAGGTGTAGCTTAAGCCTTAACCTTCTTACAGAGAAGCCTTCTCTGA	83607
Qy	14161	CCATTACACCTCTTCTTAATTAGGTTTACCTCTGTTTGTAGTTTCTTTGTTTTTTTT	14220
Db	83608	CCATTACACCTCTTCTTAATTAGGTTTACCTCTGTTTGTAGTTTCTTTGTTTTTTTT	83667
Qy	14221	TTTTTTTTTTTTTTTAAATATGATTTCTTACTGTCTACCCAGGCTGGAGTGCAGTCACT	14280
Db	83668	TTTTTTTTTTTTTTTAAATATGATTTCTTACTGTCTACCCAGGCTGGAGTGCAGTCACT	83727
Qy	14281	GATCTTGGCTCACTGCAACCTCGGCTCCGGGCAATCAATTTCTCTGCTCAGCCTCCTCC	14340
Db	83728	GATCTTGGCTCACTGCAACCTCGGCTCCGGGCAATCAATTTCTCTGCTCAGCCTCCTCC	83787
Qy	14341	AAGTAGCTGGGGTTACAGGTGTGCACACACACATCTGGCTTAATTTTGTGTTTTAGTGC	14400
Db	83788	AAGTAGCTGGGGTTACAGGTGTGCACACACACATCTGGCTTAATTTTGTGTTTTAGTGC	83847
Qy	14401	CCAGCTAAATTTTGTATTTTTTAGTAGAGCGGGGTTTCCACCTGTTGGCCAGGCTGATCT	14460
Db	83848	CCAGCTAAATTTTGTATTTTTTAGTAGAGCGGGGTTTCCACCTGTTGGCCAGGCTGATCT	83907
Qy	14461	CGAACTCCTGACCTCAAGTGTACCACTACCTCAGGCTCCCAAGTGTCTGGGATTAAGG	14520
Db	83908	CGAACTCCTGACCTCAAGTGTACCACTACCTCAGGCTCCCAAGTGTCTGGGATTAAGG	83967
Qy	14521	CATGAGCCACCAACCCAGCCTTAGGTTTTCCCATTTCTTTTGGGTCTGTCATCATGATGTG	14580
Db	83968	CATGAGCCACCAACCCAGCCTTAGGTTTTCCCATTTCTTTTGGGTCTGTCATCATGATGTG	84027
Qy	14581	TTACTTTTAAATGTTTCGTTTGGGCTTGCCTTCCCTACTAGACTCTAAGTGTCTGFAAAACAG	14640
Db	84028	TTACTTTTAAATGTTTCGTTTGGGCTTGCCTTCCCTACTAGACTCTAAGTGTCTGFAAAACAG	84087



QY	10261	CTCCAGCTAATTTTGTATTTTATAGATGAGTTTCCCACTGTTGGCCAGGCTG	10320
Db	79708	CTCCAGCTAATTTTGTATTTTATAGATGAGTTTCCCACTGTTGGCCAGGCTG	79767
QY	10321	GTCTTAACCTCTGACCTGAGTGATCCACCCGTCGGGCTCCCAATGCTGGGATTA	10380
Db	79768	GTCTTAACCTCTGACCTGAGTGATCCACCCGTCGGGCTCCCAATGCTGGGATTA	79827
QY	10381	TAGGCTAGAGCCAGCCAGCCGCGGTTTCTACAGTTTCTTAATCTCAAGATGTGA	10440
Db	79828	TAGGCTAGAGCCAGCCAGCCGCGGTTTCTACAGTTTCTTAATCTCAAGATGTGA	79887
QY	10441	CTTTCACAACTATGTTTGTATCTTAATCTTAATAGGGGAAAAATGTATTAAG	10500
Db	79888	CTTTCACAACTATGTTTGTATCTTAATCTTAATAGGGGAAAAATGTATTAAG	79947
QY	10501	ATGTTTAATATGATATGATGATTTTTCATTAATCTTAATGCTTGAAGGAAATTTGCT	10560
Db	79948	ATGTTTAATATGATATGATGATTTTTCATTAATCTTAATGCTTGAAGGAAATTTGCT	80007
QY	10561	GTCCAGCTGAATGCTATCTTGGTGTAGTGGCTGTCAACCTTGAGAGCATTTCAAT	10620
Db	80008	GTCCAGCTGAATGCTATCTTGGTGTAGTGGCTGTCAACCTTGAGAGCATTTCAAT	80067
QY	10621	TTTCAGGTAATCTCCAGGAAACCCTTGGGCTTAACCTGAAAGAGCTGTCATNT	10680
Db	80068	TTTCAGGTAATCTCCAGGAAACCCTTGGGCTTAACCTGAAAGAGCTGTCATNT	80127
QY	10681	GTCCCTCACTGGCTTCTCAAGCTAGTGAATTTGATCAAGTTAACTTACCAAGTGTG	10740
Db	80128	GTCCCTCACTGGCTTCTCAAGCTAGTGAATTTGATCAAGTTAACTTACCAAGTGTG	80187
QY	10741	GGTTCAGCTCAGGTAAGAGATTAATGATTAATAGTTAATAGTACCTTATTAATCT	10800
Db	80188	GGTTCAGCTCAGGTAAGAGATTAATGATTAATAGTTAATAGTACCTTATTAATCT	80247
QY	10801	CTTTGTTAAAAAATTTATTTTATAGAGACATCTCATTTCTTCCAGGTTAGAGTGC	10860
Db	80248	CTTTGTTAAAAAATTTATTTTATAGAGACATCTCATTTCTTCCAGGTTAGAGTGC	80307
QY	10861	AGTGACACAATCATAGCTACATGTCCTTGAACCTCGGGCTTACAGATCTCTCTCT	10920
Db	80308	AGTGACACAATCATAGCTACATGTCCTTGAACCTCGGGCTTACAGATCTCTCTCT	80367
QY	10921	CAACCTTGAATAGCTGGGACATTAACAGGATATGCCAACCTGCCAGCTAATTTT	10980
Db	80368	CAACCTTGAATAGCTGGGACATTAACAGGATATGCCAACCTGCCAGCTAATTTT	80427
QY	10981	TTATTTAGTAGAGACAGGCTTGTCTGTGCTTGGCCAGCTGATCTTGACCTGCGCT	11040
Db	80428	TTATTTAGTAGAGACAGGCTTGTCTGTGCTTGGCCAGCTGATCTTGACCTGCGCT	80487
QY	11041	CAAGTAATCTCCACCTTGGCTCCCAAAATGCTGGGGTCAAGGGCTCAGCCACATGC	11100
Db	80488	CAAGTAATCTCCACCTTGGCTCCCAAAATGCTGGGGTCAAGGGCTCAGCCACATGC	80547
QY	11101	CCAGCTGTATACAGTTGATGCTGCTTCTTAACTAAGTTTGTATGACTTCAATTT	11160
Db	80548	CCAGCTGTATACAGTTGATGCTGCTTCTTAACTAAGTTTGTATGACTTCAATTT	80607
QY	11161	TATCCATGAGGTTTAAAGATATATGTTTGTCTTCTTCACTCACTCAACAGTTCC	11220
Db	80608	TATCCATGAGGTTTAAAGATATATGTTTGTCTTCTTCACTCACTCAACAGTTCC	80667
QY	11221	AAGCAAAAGTAGCCCTTGTGGGCAAAAGAACTGAGAGGAGGCTAGATATTCTTC	11280
Db	80668	AAGCAAAAGTAGCCCTTGTGGGCAAAAGAACTGAGAGGAGGCTAGATATTCTTC	80727
QY	11281	CCCTTGTGTTCCCTACATGCTTTTGGAGAGATTAAGAAAGACATTTGAAATGACAC	11340
Db	80728	CCCTTGTGTTCCCTACATGCTTTTGGAGAGATTAAGAAAGACATTTGAAATGACAC	80787
QY	11341	TGAGGATTAAGAAATTCAGCCAGTCCGGTGCCTCAGCCACGACTTACAGAGCTGAG	11400

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Db	80788	TGAGGATTAAGAAATTCAGCCAGTCCGGTGCCTCAGCCACGACTTTAGAGACTGAG	80847
QY	11401	TGGTGCAATGCTTGAACCTCAGAGAGTTGAGACACAGCTGGGAAACATGTAATCCCA	11460
Db	80848	TGGTGCAATGCTTGAACCTCAGAGAGTTGAGACACAGCTGGGAAACATGTAATCCCA	80907
QY	11461	ACTTAAAAAAGAAAAAAGAAAAAAGAAAAAATAGTGCCTGAGAAATCCAGG	11520
Db	80908	ACTTAAAAAAGAAAAAAGAAAAAAGAAAAAATAGTGCCTGAGAAATCCAGG	80967
QY	11521	AGAAATAGTGTCTGCGTGGGCGGTGGTATAGCTTAATCTGAGCACTTTGGGAG	11580
Db	80968	AGAAATAGTGTCTGCGTGGGCGGTGGTATAGCTTAATCTGAGCACTTTGGGAG	81027
QY	11581	GCTGAGGACGTGGATCACTTAAGGTCAGGAGTTGAGACACAGACTGCAAAAGTGA	11640
Db	81028	GCTGAGGACGTGGATCACTTAAGGTCAGGAGTTGAGACACAGACTGCAAAAGTGA	81087
QY	11641	AACCCGCTCTCTACTAAAAAATACAAATACAGCCAGCTTGGTGGCAGCTGCTGA	11700
Db	81088	AACCCGCTCTCTACTAAAAAATACAAATACAGCCAGCTTGGTGGCAGCTGCTGA	81147
QY	11701	GTCCAGCTACTTGGGAGGCTGAGACAAAGAAATTTGCTTAACCTGGGAGGACAGTTG	11760
Db	81148	GTCCAGCTACTTGGGAGGCTGAGACAAAGAAATTTGCTTAACCTGGGAGGACAGTTG	81207
QY	11761	CAGTGAGCCGAGATCAGCCAGCTGCTCCAGCATGGGCGACAGAGTACCTCTCTC	11820
Db	81208	CAGTGAGCCGAGATCAGCCAGCTGCTCCAGCATGGGCGACAGAGTACCTCTCTC	81267
QY	11821	AAAAAAGAAAAAAGAAAAAAGTTCGTGATTAAGCTGCTGGGAGAAAGCACTCT	11880
Db	81268	AAAAAAGAAAAAAGAAAAAAGTTCGTGATTAAGCTGCTGGGAGAAAGCACTCT	81327
QY	11881	TTGGAGAAAGAAAACTTGAGTCAAACTCTGCTTACTTTCTTATGCCAGATGCTGC	11940
Db	81328	TTGGAGAAAGAAAACTTGAGTCAAACTCTGCTTACTTTCTTATGCCAGATGCTGC	81387
QY	11941	TATTAAGTAAGCTAAGCTTGTATCTGTAACAGATTTGATGAAGTTAAATCTGA	12000
Db	81388	TATTAAGTAAGCTAAGCTTGTATCTGTAACAGATTTGATGAAGTTAAATCTGA	81447
QY	12001	CCCATATGCCCTTTGGCCAAAGCACTGAGCCAGCAGCATGATTTTAAATGAATTT	12060
Db	81448	CCCATATGCCCTTTGGCCAAAGCACTGAGCCAGCAGCATGATTTTAAATGAATTT	81507
QY	12061	GAAGCCCGAGACCTGACATATGGCTGTAGAGAGCACTGACCTTACCTGCAAAAT	12120
Db	81508	GAAGCCCGAGACCTGACATATGGCTGTAGAGAGCACTGACCTTACCTGCAAAAT	81567
QY	12121	TACATATTTGAGGAGATGAGACCCATGAGTGTGGAGATAGGTTAGGCTCAGTCACT	12180
Db	81568	TACATATTTGAGGAGATGAGACCCATGAGTGTGGAGATAGGTTAGGCTCAGTCACT	81627
QY	12181	GTTTTGTCTTCTGCTTCCATATCATCTGATGAGGATACATGATTAACCTCTTAA	12240
Db	81628	GTTTTGTCTTCTGCTTCCATATCATCTGATGAGGATACATGATTAACCTCTTAA	81687
QY	12241	AACAGTCTCTAATTTCAATCTAATTAATCACAGTTGACAGCCATATGAGGCTCTTC	12300
Db	81688	AACAGTCTCTAATTTCAATCTAATTAATCACAGTTGACAGCCATATGAGGCTCTTC	81747
QY	12301	CATTAACCAATTAATTTATTCACCAAGCTGTAGAGCAAGGTAAGTCAAGATCTGTGG	12360
Db	81748	CATTAACCAATTAATTTATTCACCAAGCTGTAGAGCAAGGTAAGTCAAGATCTGTGG	81807
QY	12361	CATCCCTCATTTTCTCAACTGCTTCTCAAACTCTCTCTGAGAGTTTCAAT	12420
Db	81808	CATCCCTCATTTTCTCAACTGCTTCTCAAACTCTCTCTGAGAGTTTCAAT	81867
QY	12421	GCTCAGGCTGGAGACTTTTACGGGCTGTTTGTATCTCTAGGGTATATCT	12480



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OY 5881 AGCGTAGCAGAGCAATTCGCTGAACCCGGGAGAGGAGTTGCAAGTAGAGATCA 5940
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Db 75328 AGCGTAGCAGAGCAATTCGCTGAACCCGGGAGAGGAGTTGCAAGTAGAGATCA 75387
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OY 5941 TGGCATTCAGCTCAGCCTGGGGGACAGAGCGGAGATCCATCTCAAAAAAAAAAAAAA 6000
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Db 75388 TGGCATTCAGCTCAGCCTGGGGGACAGAGCGGAGATCCATCTCAAAAAAAAAAAAAA 75447
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OY 6001 AAGCAAAAGTTACAAATGATATTTGTCAGATTTCAGATGGCAATGGCAACAAACGA 6060
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Db 75448 AAGCAAAAGTTACAAATGATATTTGTCAGATTTCAGATGGCAATGGCAACAAACGA 75507
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OY 6061 TAAAGCGCTATGGAAGACCTAGCTGTAACCTGTTTCTGTAATGATGGGAAAGTTTA 6120
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OY 6121 CATCATATATATAGTAAATGATAGGTTATTTTGTCTGTCGCAAGCCTCTCTCT 6180
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Db 75568 CATCATATATATAGTAAATGATAGGTTATTTTGTCTGTCGCAAGCCTCTCTCT 75627
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OY 6181 GAGGACTGCGGAATGCTGATTAACCTCTTGTGTTAGATGATGCTCCAGATGGAC 6240
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Db 75628 GAGGACTGCGGAATGCTGATTAACCTCTTGTGTTAGATGATGCTCCAGATGGAC 75687
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OY 6241 TTGTTCCACAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 6300
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Db 75748 AGGTGAGAGAGAGAGCAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 75807
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OY 6361 GTACCTCAGACCTATTTATGAGAGCTGCTTACCTGTCATGATGATGATGATGAT 6420
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OY 6421 AGCTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6480
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Db 75868 AGCTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 75927
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OY 6481 GCTATCTTTTGTGTTTGAAGAGCTATACATAGACAGTCTCTTCACTGTTGTCGTA 6540
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Db 75928 GCTATCTTTTGTGTTTGAAGAGCTATACATAGACAGTCTCTTCACTGTTGTCGTA 75987
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OY 6541 ATTAATTTTTTTTGTCTAAAGCAGCAAGGCTGCAAAAAGAAACAAATACCCAGGA 6600
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OY 6601 ACTCTAGTTTCACAATCCAGGCCATGTAATATTAGAGAGTTATGACTTTTATGCG 6660
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OY 6841 CCCCGTAGATTTAGTGTGATGAGAGCTTGGAGAGATCTTAACCTTACAGAGCTGTTGCA 6900
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OY 6901 GCTTAATCATTAAGCTTGTCTAATATACCTTAAAGAGCTTACAGAGAGAGAGAGAG 6960
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Db 76348 GCTTAATCATTAAGCTTGTCTAATATACCTTAAAGAGCTTACAGAGAGAGAGAGAG 76407
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OY 6961 ACAGTGTACTTAATCTTACAGACTATTGGCAGTAGACAGCTATATCATGATATATCTGG 7020
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Db	73108	AACATTTTCTATGATGTTAAAGAAAGTTTATATAGATTAATTCATAAGATTAATTAATA	73167
QY	3721	TTATATGTATGTAATGATTTGGAATTCACATATAGGACATCATATGATCCCTATTAG	3780
Db	73168	TTATATGTATGTAATGATTTGGAATTCACATATAGGACATCATATGATCCCTATTAG	73227
QY	3781	ATTATATGTTGCTTTTATCCCATCATTTTCAATTTAAGATTCACITTTGGTTCATA	3840
Db	73228	ATTATATGTTGCTTTTATCCCATCATTTTCAATTTAAGATTCACITTTGGTTCATA	73287
QY	3841	TTTATACCTATCAAAATTAACCTCTACATACAGCTTTTAGGTTATCCATAGATTTTCTAAGG	3900
Db	73288	TTTATACCTATCAAAATTAACCTCTACATACAGCTTTTAGGTTATCCATAGATTTTCTAAGG	73347
QY	3901	TAGTGGTTCTTCTCTCAGAGCTTTTGTTCAAATAAATCTTTTAAAGATGACAGATA	3960
Db	73348	TAGTGGTTCTTCTCTCAGAGCTTTTGTTCAAATAAATCTTTTAAAGATGACAGATA	73407
QY	3961	AAAGTTGAAGCTGTTCAAGATGTAAGTGGAAAGTTTGGAAACTTTAGTACTAGTGGCC	4020
Db	73408	AAAGTTGAAGCTGTTCAAGATGTAAGTGGAAAGTTTGGAAACTTTAGTACTAGTGGCC	73467
QY	4021	TCCTGAAGGAATTTTCCAGGAAGCTTAGGATTTAGAACAACTTAGCTTTAAGAAATACAG	4080
Db	73468	TCCTGAAGGAATTTTCCAGGAAGCTTAGGATTTAGAACAACTTAGCTTTAAGAAATACAG	73527
QY	4081	TATAGGCTGGGCTGGCTCATGCTCTAATCCAGCAGCTTTGGAGGCTGAGATGGA	4140
Db	73528	TATAGGCTGGGCTGGCTCATGCTCTAATCCAGCAGCTTTGGAGGCTGAGATGGA	73587
QY	4141	CAGATCCCTGAGGTCAGAGTTCAAGACAGCTGGCCCAAGCTGTGAAGCCCTATCTC	4200
Db	73588	CAGATCCCTGAGGTCAGAGTTCAAGACAGCTGGCCCAAGCTGTGAAGCCCTATCTC	73647
QY	4201	TACTAAAAAACAATAATAGCCAGCATGTTGGCAGCAGCTGTAATCCAGCTACTCG	4260
Db	73648	TACTAAAAAACAATAATAGCCAGCATGTTGGCAGCAGCTGTAATCCAGCTACTCG	73707
QY	4261	GGAGGTTGAGGATGAGAACTACTTGAACCCAGGAGTGGAGGTTGCACTGAGCCGAGAT	4320
Db	73708	GGAGGTTGAGGATGAGAACTACTTGAACCCAGGAGTGGAGGTTGCACTGAGCCGAGAT	73767
QY	4321	GCATCTCTGCACTCCAGCTAGGCGACAGAGGACATTCATCTCAAAAAAATAAAAA	4380
Db	73768	GCATCTCTGCACTCCAGCTAGGCGACAGAGGACATTCATCTCAAAAAAATAAAAA	73827
QY	4381	AGAGAAATPACAGTATAGTCTTTCGATAAAATCAGTTTTCAGAAAGCCACCAACTTCT	4440
Db	73828	AGAGAAATPACAGTATAGTCTTTCGATAAAATCAGTTTTCAGAAAGCCACCAACTTCT	73887
QY	4441	GCCATTTTGGACCAATGGGACCAAGGTGACTTTTGAATCCAGGTTGACACAGATTTTAT	4500
Db	73888	GCCATTTTGGACCAATGGGACCAAGGTGACTTTTGAATCCAGGTTGACACAGATTTAT	73947
QY	4501	CTCCGGGGAGCTGAAGTCATAAGAACTAGTCTGTTTGTATTTACAGGAGCTCTGAG	4560
Db	73948	CTCCGGGGAGCTGAAGTCATAAGAACTAGTCTGTTTGTATTTACAGGAGCTCTGAG	74007
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AUTHORS Howden, P.  
TITLE Direct Submission  
JOURNAL Submitted (06-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone  
requests: clonerequest@sanger.ac.uk

## COMMENT

On Sep 19, 2000 this sequence version replaced gi:9714820.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:  
Em: EMBL, Sw: SWISSPROT, Tr: TREMBL, Wp: WORMPEP, Information  
on the WORMPEP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping  
Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr1>  
This sequence is the entire insert of clone RP11-43507 The true  
left end of clone RP1-6283 is at 123829 in this sequence. The true  
right end of clone RP4-555P23 is at 81044 in this sequence. This  
sequence has been finished according to sequence map criteria as  
follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated repeat sequence elements. Where the sequence is  
ambiguous, there is an annotation using the 'unsure' feature key.  
RP11-43507 is from the library RPCR-11.2 constructed by the group  
of Piter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
VECTOR: pBac3.6.

## FEATURES

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 14:49:43 ; Search time 70178 Seconds  
(Without alignments)  
11958.699 Million cell updates/sec

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Perfect score: 28837  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
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22: em.ov.\*  
23: em.pat.\*  
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25: em.pl.\*  
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35: em.htg\_rod.\*  
36: em.htg\_mam.\*  
37: em.htg\_vrt.\*  
38: em.sy.\*  
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40: em.htgo\_mus.\*  
41: em.htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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3	1166	4.0	111862	2	AL139143 Homo sapi
4	484	1.7	2934	9	AK096303 Homo sapi
5	361	1.3	2579	9	BC026909 Homo sapi
6	340	1.2	466	6	AX333105 Sequence
7	340	1.2	466	11	G30470 human STS S
8	299	1.0	2394	9	AK096466 Homo sapi
9	291	1.0	4756	9	AF297866 Homo sapi
10	247	0.9	111744	2	AC099686 Homo sapi
11	247	0.9	161613	2	AC023947 Homo sapi
12	246	0.9	110000	2	AC092450_4
13	246	0.9	110000	2	AC092450_5
14	245	0.8	80485	9	HSJ231P7P
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23	242	0.8	79815	9	AC005212
24	242	0.8	118958	9	AC092579
25	242	0.8	176077	2	AC019039
26	242	0.8	185281	2	AC011214
27	242	0.8	189008	2	AP001491
28	242	0.8	207295	9	AL353572
29	242	0.8	207818	9	AC019206
30	241	0.8	102479	9	AC115107
31	241	0.8	108048	9	AC115108
32	241	0.8	117051	9	AC115106
33	241	0.8	138993	2	AC087653
34	241	0.8	186428	9	AC016355
35	239	0.8	39441	9	AC005565
36	239	0.8	41073	9	AC005567
37	239	0.8	122783	2	AF238376
38	239	0.8	142839	9	AL356218
39	239	0.8	155221	9	AC069335
40	239	0.8	166553	2	AL844523
41	239	0.8	187656	2	AC020564
42	239	0.8	234626	2	AC009095
43	238	0.8	165221	9	AP000457
44	238	0.8	176851	2	AC016372
45	238	0.8	290766	2	AL583862

# ALIGNMENTS

RESULT 1  
AL354864  
LOCUS  
DEFINITION

194296 bp DNA linear PRI 04-APR-2001  
Human DNA sequence from clone RP11-435D7 on chromosome 1. Contains  
ESTs, STSS, GSSs and Cpg Islands. Contains a novel gene and the 5'  
part of the PSMB2 gene for Proteasome (prosome, macropain) subunit  
2, beta type, complete sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AL354864  
AL354864.16 GI:10185566  
HTG; Cpg Island; macropain; prosome; proteasome; PSMB2.  
human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 194296)

Pred. No. is the number of results predicted by chance to have a



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Db      91697 CCACCACCGCCGGCTAAATTTTGTATTTTAGTAGACGGGTTTCACCATGTTAGCC 91756
OY      27674 AGGATGGTCTTGCATCTCTGACCTCGTGCATCCGCCGCTCGGCTCCC 27722
Db      91757 AGGATGGTCTTGCATCTCTGACCTCGTGCATCCGCCGCTCGGCTCCC 91805

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## RESULT 15

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AP000729
LOCUS      Homo sapiens genomic DNA, chromosome 11 clone:RP11-699D4, complete
DEFINITION
ACCESSION AP000729
VERSION   AP000729.4 GI:22415810
KEYWORDS  HTG.
SOURCE    Homo sapiens DNA, clone:RP11-699D4.
ORGANISM  Homo sapiens

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REFERENCE
AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
           Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE     Homo sapiens genomic DNA
JOURNAL   Published Only in Database (1999)

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REFERENCE
AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
           Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE     Direct Submission
JOURNAL   Submitted (16-NOV-1999) Masahira Hattori, The Institute of Physical

```

```

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT   On Aug 21, 2002 this sequence version replaced gi:11071942.
FEATURES
SOURCE    Location/Qualifiers

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1. .160535
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   /db_xref="taxon:9606"
   /chromosome="11"
   /map="11q"
   /clone="RP11-699D4"

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BASE COUNT 39840 a 39815 c 41519 g 39361 t
ORIGIN

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Query Match      0.4%; Score 109; DB 9; Length 160535;
Best Local Similarity 100.0%; Pred No. 1.5e-44;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      27614 CCACCACCGCCGGCTAAATTTTGTATTTTAGTAGACGGGTTTCACCATGTTAGCC 27673
Db      75532 CCACCACCGCCGGCTAAATTTTGTATTTTAGTAGACGGGTTTCACCATGTTAGCC 75591
OY      27674 AGGATGGTCTTGCATCTCTGACCTCGTGCATCCGCCGCTCGGCTCCC 27722
Db      75592 AGGATGGTCTTGCATCTCTGACCTCGTGCATCCGCCGCTCGGCTCCC 75640

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Search completed: June 24, 2003, 10:33:52
Job time : 58874 secs

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60057 63347 contig of 1291 bp in length
63448 66289 contig of 2842 bp in length
66390 69592 contig of 3203 bp in length
69693 72010 contig of 3218 bp in length
72111 75133 contig of 3023 bp in length
75234 77770 contig of 2537 bp in length
77871 81172 contig of 3302 bp in length
81273 83633 contig of 2361 bp in length
81273 83633 contig of 2361 bp in length

Sequence updated (26-May-2000).
NOTE: This is a 'working draft' sequence. It currently
* consists of 40 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 12428: contig of 12428 bp in length
12429 12528: gap of 100 bp
12529 20628: contig of 8100 bp in length
20629 20728: gap of 100 bp
20729 29692: contig of 8964 bp in length
29693 29792: gap of 100 bp
29793 38212: contig of 8420 bp in length
38213 38312: gap of 100 bp
38313 45303: contig of 6991 bp in length
45304 45403: gap of 100 bp
45404 49522: contig of 4119 bp in length
49523 49622: gap of 100 bp
49623 52789: contig of 3167 bp in length
52790 52889: gap of 100 bp
52890 56364: contig of 3475 bp in length
56365 56464: gap of 100 bp
56465 59956: contig of 3492 bp in length
59957 60056: gap of 100 bp
60057 63347: contig of 3291 bp in length
63348 63447: gap of 100 bp
63448 66289: contig of 2842 bp in length
66290 66389: gap of 100 bp
66390 69592: contig of 3203 bp in length
69593 69692: gap of 100 bp
69693 72010: contig of 2318 bp in length
72011 72110: gap of 100 bp
72111 75133: contig of 3023 bp in length
75134 75233: gap of 100 bp
75234 77770: contig of 2537 bp in length
77771 77870: gap of 100 bp
77871 81172: contig of 3302 bp in length
81173 81272: gap of 100 bp
81273 83633: contig of 2361 bp in length

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83634 83733: gap of 100 bp
83734 86316: contig of 2583 bp in length
86317 86416: gap of 100 bp
86417 89734: contig of 3318 bp in length
89735 89834: gap of 100 bp
89835 93303: contig of 3469 bp in length
93304 93403: gap of 100 bp
93404 95990: contig of 2587 bp in length
95991 96090: gap of 100 bp
96091 96493: contig of 2403 bp in length
96494 96593: gap of 100 bp
96594 101329: contig of 2736 bp in length
101330 101429: gap of 100 bp
101430 102985: contig of 1556 bp in length
102986 103085: gap of 100 bp
103086 104913: contig of 1828 bp in length
104914 105013: gap of 100 bp
105014 107643: contig of 2630 bp in length
107644 107743: gap of 100 bp
107744 109302: contig of 1559 bp in length
109303 109402: gap of 100 bp
109403 111110: contig of 1708 bp in length
111111 112210: gap of 100 bp
112211 112850: contig of 1640 bp in length
112851 112950: gap of 100 bp
112951 114294: contig of 1344 bp in length
114295 114394: gap of 100 bp
114395 115578: contig of 1184 bp in length
115579 115678: gap of 100 bp
115679 117097: contig of 1419 bp in length
117098 117197: gap of 100 bp
117198 118741: contig of 1544 bp in length
118742 118841: gap of 100 bp
118842 120316: contig of 1475 bp in length
120317 120416: gap of 100 bp
120417 121928: contig of 1512 bp in length
121929 122028: gap of 100 bp
122029 123611: contig of 1583 bp in length
123612 123711: gap of 100 bp
123712 125176: contig of 1465 bp in length
125177 125276: gap of 100 bp
125277 126313: contig of 1037 bp in length
126314 126413: gap of 100 bp
126414 126497: contig of 84 bp in length
126498 126597: gap of 100 bp
126598 127661: contig of 1064 bp in length.

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## FEATURES

## source

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   /db_xref="taxon:9606"
   /chromosome="11"
   /map="11q13"
   /clone="Rp11-655A22"
1. 12428
   /note="assembly-fragment"
misc-feature
   /note="assembly-fragment"
12529..20628
   /note="assembly-fragment"
20729..29692
   /note="assembly-fragment"
29793..38212
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38313..45303
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45404..49522
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49623..52789
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misc-feature
misc-feature
misc-feature

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Query Match 0.4%; Score 109; DB 2; Length 127661;

Best Local Similarity 100.0%; Pred. No. 1,5e-44;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27614 CCACCACCCCGCGCTATTGTTGATTGTTAGTAGACACGGGTTCCACCATGTAGCC 27673

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/rpt_family="(TTTC)n"
complement(13406..13428)
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complement(13429..13690)
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complement(13691..13871)
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complement(13882..14103)
/rpt_family="L1MED"
14104..14309
/rpt_family="(TA)n"
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/rpt_family="L1MED"
complement(14330..14634)
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15047..15460
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15994..16107
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complement(17567..18296)
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complement(18309..18781)
/rpt_family="L1MB2"
18792..18813
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complement(18817..19100)
/rpt_family="AluSg"
complement(19114..19305)
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complement(19306..19582)
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complement(21038..21438)
/rpt_family="MSTA"
complement(21439..21616)
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21617..22779
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complement(22929..23054)
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complement(23047..23448)
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complement(23527..23840)
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/rpt_family="L1MD1"
complement(24063..24332)
/rpt_family="AluJo"
complement(24333..24436)
24437..24483
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complement(24484..25973)

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Best Local Similarity 100.0%; Pred. No. 4.3e-46;

Matches 112: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29776 CAGCCTGACCAACATGGTGAACCCCTCTCTACTAATAACAAAAATTAGCTGGCATG 29835  
|||||  
Db 191326 CAGCCTGACCAACATGGTGAACCCCTCTCTACTAATAACAAAAATTAGCTGGCATG 191385  
|||||

QY 29836 GTGGCGCATGCTCTTAATCCAGCTACTTGGGAGGCTGAGCGAGGAATG 29887  
|||||  
Db 191386 GTGGCGCATGCTCTTAATCCAGCTACTTGGGAGGCTGAGCGAGGAATG 191437  
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RESULT 14  
AP001261  
LOCUS AP001261 127661 bp DNA linear HTG 31-MAY-2000  
DEFINITION Homo sapiens chromosome 11 clone RP11-655A22 map 11q13, WORKING  
DRAFT SEQUENCE, 40 unordered pieces.  
ACCESSION AP001261  
VERSION AP001261.2 GI:8131598  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE Homo sapiens DNA, clone:RP11-655A22.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 127661)  
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
Homo sapiens 127,661 genomic DNA of 11q13  
2 (bases 1 to 127661)  
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
Submitted (23-FEB-2000) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,  
Japan (E-mail:hattori@gscenter.riken.go.jp,  
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,  
Fax:81-42-778-9924)  
On May 31, 2000 this sequence version replaced gi:7106129.  
----- Genome Center  
Center: RIKEN Genomic Sciences Center(GSC)  
Center code: RIKEN  
Web site: http://hgp.gsc.riken.go.jp/  
Contact: hattori@gscenter.riken.go.jp  
----- Project Information  
Center project name: HumDraft11  
Center clone name: RP11-655A22  
----- Summary Statistics  
Sequencing vector: PCR products; 100% of reads  
Chemistry: Dye-terminator ET-amersham; 100% of reads  
Assembly program: Phrap; version 0.950329  
Consensus quality: 105777 bases at least Q40  
Consensus quality: 115033 bases at least Q30  
Consensus quality: 120045 bases at least Q20  
Insert size: 123761; sum-of-contigs  
Quality coverage: 4.16x in Q20 bases; sum-of-contigs  
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NOTE: This is a 'working draft' sequence. It currently consists of  
40 contigs. The true order of the pieces is not known and the  
order in this sequence record is arbitrary. Gaps between the  
contigs are represented as runs N, but the exact sizes of the gaps  
are unknown. This record will be updated with the finished sequence  
as soon as it is available and the accession number will be  
preserved  
1 12428 contig of 12428 bp in length  
12529 26628 contig of 8100 bp in length  
20729 29692 contig of 8964 bp in length  
29793 38212 contig of 8420 bp in length  
38313 45303 contig of 6991 bp in length  
45404 49522 contig of 4119 bp in length  
49623 52789 contig of 3167 bp in length  
52890 56364 contig of 3475 bp in length  
56465 59956 contig of 3492 bp in length



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- QY      10267 CAAAACGTGT 10275
Db        |||||||
          403 CAAAACGTGT 411

RESULT 10
AX069706
LOCUS    AX069706          386 bp      DNA      linear      PAT 25-JAN-2001
DEFINITION Sequence 178 from Patent WO0102568.
ACCESSION AX069706
VERSION   AX069706.1 GI:12579491
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS   Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.,
           Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
           Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
           Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and Strache-Crain,B.
TITLE     Human genes and gene expression products
JOURNAL   Patent: WO 0102568-A 178 11-JAN-2001;
           CHIRON CORPORATION (US) ; HYSEQ, INC. (US)
FEATURES
source    1..386
           /organism="Homo sapiens"
misc_feature 1..386
           /db_xref="taxon:9606"
BASE COUNT 128 a 76 c 116 g 65 t 1 others
ORIGIN

Query Match      0.4%; Score 135; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10087 AGATTGAGTGAAGAGATATTTGTAAGTGAAGAGTTGAAAACAGGAGGTTCTACAAGA 10146
Db      |||||||
          251 AGATTGAGTGAAGAGATATTTGTAAGTGAAGAGTTGAAAACAGGAGGTTCTACAAGA 310

QY      10147 CAGTGATTCGAAACAGAGGACACAAATGCTCTCCAGAGAAAACACTATGACAGTGC 10206
Db      |||||||
          311 CAGTGATTCGAAACAGAGGACACAAATGCTCTCCAGAGAAAACACTATGACAGTGC 370

QY      10207 CGAGGAGGAAATAA 10221
Db      |||||||
          371 CGAGGAGGAAATAA 385

RESULT 11
AX071923
LOCUS    AX071923          406 bp      DNA      linear      PAT 25-JAN-2001
DEFINITION Sequence 2395 from Patent WO0102568.
ACCESSION AX071923
VERSION   AX071923.1 GI:12582274
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS   Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.,
           Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
           Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
           Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and Strache-Crain,B.
TITLE     Human genes and gene expression products
JOURNAL   Patent: WO 0102568-A 2395 11-JAN-2001;
           CHIRON CORPORATION (US) ; HYSEQ, INC. (US)
FEATURES
source    1..406
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misc_feature 1..406
           /db_xref="taxon:9606"
BASE COUNT 128 a 76 c 116 g 65 t 1 others
ORIGIN

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Best Local Similarity 99.5%; Pred. No. 5.3e-57;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10087 AGATTGAGTGAAGAGATATTTGTAAGTGAAGAGTTGAAAACAGGAGGTTCTACAAGA 10146
Db      |||||||
          223 AGATTGAGTGAAGAGATATTTGTAAGTGAAGAGTTGAAAACAGGAGGTTCTACAAGA 282

QY      10147 CAGTGATTCGAAACAGAGGACACAAATGCTCTCCAGAGAAAACACTATGACAGTGC 10206
Db      |||||||
          283 CAGTGATTCGAAACAGAGGACACAAATGCTCTCCAGAGAAAACACTATGACAGTGC 342

QY      10207 CGAGGAGGAAATAAAGAGAAATTTATATGCTGGGAAAAATACAAAAGGATTTA 10266
Db      |||||||
          343 CGAGGAGGAAATAAAGAGAAATTTATATGCTGGGAAAAATACAAAAGGATTTA 402

QY      10267 CAAA 10270
Db      |||||
          403 CAAA 406

BASE COUNT 142 a 73 c 115 g 76 t
ORIGIN

Query Match      0.4%; Score 133; DB 6; Length 406;
Best Local Similarity 99.5%; Pred. No. 5.3e-57;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10087 AGATTGAGTGAAGAGATATTTGTAAGTGAAGAGTTGAAAACAGGAGGTTCTACAAGA 10146
Db      |||||||
          223 AGATTGAGTGAAGAGATATTTGTAAGTGAAGAGTTGAAAACAGGAGGTTCTACAAGA 282

QY      10147 CAGTGATTCGAAACAGAGGACACAAATGCTCTCCAGAGAAAACACTATGACAGTGC 10206
Db      |||||||
          283 CAGTGATTCGAAACAGAGGACACAAATGCTCTCCAGAGAAAACACTATGACAGTGC 342

QY      10207 CGAGGAGGAAATAAAGAGAAATTTATATGCTGGGAAAAATACAAAAGGATTTA 10266
Db      |||||||
          343 CGAGGAGGAAATAAAGAGAAATTTATATGCTGGGAAAAATACAAAAGGATTTA 402

QY      10267 CAAA 10270
Db      |||||
          403 CAAA 406

RESULT 12
AC005848/c
LOCUS    AC005848          174562 bp      DNA      linear      HTG 30-AUG-2001
DEFINITION Homo sapiens chromosome 11 clone CIT987SK-1012F4, 6 unordered
           pieces.
ACCESSION AC005848
VERSION   AC005848.1 GI:3779014
KEYWORDS  HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE    Homo sapiens.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS   Smith,D.R.
TITLE     Sequencing of Human Chromosome 10
JOURNAL   Unpublished
REFERENCE
AUTHORS   Smith,D.R.
TITLE     2 (bases 1 to 174562)
JOURNAL   Direct Submission
           Submitted (22-OCT-1998) Genome Therapeutics Corporation, 100 Beaver
           Street, Waltham, MA 02154, USA
COMMENT   * NOTE: This is a 'working draft' sequence. It currently
           * consists of 6 contigs. The true order of the pieces
           * is not known and their order in this sequence record is
           * arbitrary. Gaps between the contigs are represented as
           * runs of N, but the exact sizes of the gaps are unknown.
           * This record will be updated with the finished sequence.
           * as soon as it is available and the accession number will
           * be preserved.
           * 1
           * 4561: contig of 4561 bp in length
           * 4562 19077: gap of unknown length
           * 4563 30350: contig of 11273 bp in length
           * 4564 30351 44866: gap of unknown length
           * 4565 44867 58909: contig of 14043 bp in length
           * 4566 58910 73424: gap of unknown length
           * 4567 73425 90412: contig of 16988 bp in length
           * 4568 90413 104927: gap of unknown length
           * 4569 104928 130554: contig of 25627 bp in length
           * 4570 130555 145069: gap of unknown length
           * 4571 145070 174562: contig of 29493 bp in length.
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           * Location/Qualifiers
           * 1..174562
           * /organism="Homo sapiens"
           * /db_xref="taxon:9606"
           * /chromosome="11"
           * /clone="CIT987SK-1012F4"
BASE COUNT 21150 a 29998 c 29519 g 21315 t 72580 others
ORIGIN

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QY 10087 AGATTGATGAAAGATATTTTAACTAAGAAAGTTCAGAAAGAGAGGTTCTACAGCA 10146  
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Db 226 AGATTGATGAAAGATATTTTAACTAAGAAAGTTCAGAAAGAGAGGTTCTACAGCA 285  
QY 10147 CAGTGATTCGGAACAGAGACACAAATGCTCTCCAGAGAAAGTCTATGACAGTGC 10206  
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Db 286 CAGTGATTCGGAACAGAGACACAAATGCTCTCCAGAGAAAGTCTATGACAGTGC 345  
QY 10207 CGAGAGAGAAATTAAGAGAAATTTATGCTGGGAAAAATACAAAATCAAAAGATTTA 10266  
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Db 346 CGAGAGAGAAATTAAGAGAAATTTATGCTGGGAAAAATACAAAATCAAAAGATTTA 405  
QY 10267 CAAAAGTGGGAGACA 10283  
|||||  
Db 406 CAAAAGTGGGAGACA 422

RESULT 7  
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LOCUS  
Sequence 853 from Patent W00166753.  
ACCESSION  
AX245923  
VERSION  
AX245923.1 GI:15860597  
KEYWORDS  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 393)  
AUTHORS  
Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,  
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,  
Kassam,A., Lamson,G., Drmanac,R., Civenjakov,R., Dickson,M.,  
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and  
Stache-Crain,B.  
TITLE  
Human genes and gene expression products  
JOURNAL  
Patent: WO 0166753-A 853 13-SEP-2001;  
Chiron Corporation (US) ; Hyseq Inc. (US)  
FEATURES  
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/db\_xref="taxon:9606"  
BASE COUNT 135 a 74 c 109 g 74 t 1 others  
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Query Match 0.6%; Score 173; DB 6; Length 393;  
Best Local Similarity 100.0%; Pred. No. 8.9e-78;  
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AX245847 408 bp DNA linear PAT 28-SEP-2001  
LOCUS  
Sequence 777 from Patent W00166753.  
ACCESSION  
AX245847  
VERSION  
AX245847.1 GI:15860521.  
KEYWORDS  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 408)

AUTHORS  
Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,  
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,  
Kassam,A., Lamson,G., Drmanac,R., Civenjakov,R., Dickson,M.,  
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and  
Stache-Crain,B.  
TITLE  
Human genes and gene expression products  
JOURNAL  
Patent: WO 0166753-A 777 13-SEP-2001;  
Chiron Corporation (US) ; Hyseq Inc. (US)  
FEATURES  
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Query Match 0.5%; Score 164; DB 6; Length 408;  
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Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 364 CGAGAGAGAAATTAAGAGAAATTTATGCTGGGAAAAATCAAA 407

RESULT 9  
AX071922 411 bp DNA linear PAT 25-JAN-2001  
LOCUS  
Sequence 2394 from Patent W00102568.  
ACCESSION  
AX071922  
VERSION  
AX071922.1 GI:12582273  
KEYWORDS  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 411)  
AUTHORS  
Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.,  
Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,  
Lamson,G., Drmanac,R., Civenjakov,R., Kita,D., Garcia,V. and  
Stache-Crain,B.  
TITLE  
Human genes and gene expression products  
JOURNAL  
Patent: WO 0102568-A 2394 11-JAN-2001;  
CHIRON CORPORATION (US) ; HYSEQ, INC. (US)  
FEATURES  
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DB 2716 GTAACCTCAGCTACTCAGAGACTGAGGAGGAGATCGCTTGAACCCCTGGAGATGGAGG 2657  
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DB 2656 TTGAGTGTAGCTGAGATACATCAGCTGCACTCCAGCTGGGCAATAGAGTGAAGTGCAT 2597  
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DB 2596 CTCAAA 2590

RESULT 5  
AX246208  
LOCUS AX246208  
DEFINITION Sequence 1138 from Patent WO0166753.  
ACCESSION AX246208  
VERSION AX246208.1 GI:15860882

KEYWORDS human.  
SOURCE

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 421)

AUTHORS

Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D.,  
Sudduth-Klinger, J., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,  
Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M.,  
Drmanac, S., Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and  
Stache-Crain, B.

TITLE Human genes and gene expression products

JOURNAL Patent: WO 0166753-A 1138 13-SEP-2001;

Chiron Corporation (US); Hyseq Inc. (US)

FEATURES

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/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 153 a 72 c 111 g 85 t

ORIGIN

Query Match 0.8%; Score 231; DB 6; Length 421;

Best Local Similarity 100.0%; Pred. No. 6.7e-108;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 248 CAGTGATTCGCAACAGAGACACAAATGCCTCCAGAGAAAACTACCTATGACAGTGC 307

QY 10207 CAGAGAGGAAAAATAAGAGATTTATGCTGGGAAAAATACAAAAATCAAAAGGATTTA 10266

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RESULT 6

AX246209

LOCUS AX246209

DEFINITION Sequence 1139 from Patent WO0166753.

ACCESSION AX246209

VERSION AX246209.1 GI:15860883

KEYWORDS human.

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 422)

AUTHORS Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D.,

Sudduth-Klinger, J., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,

Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M.,

Drmanac, S., Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and

Stache-Crain, B.

TITLE Human genes and gene expression products

JOURNAL Patent: WO 0166753-A 1139 13-SEP-2001;

Chiron Corporation (US); Hyseq Inc. (US)

FEATURES

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ORIGIN

Query Match 0.7%; Score 197; DB 6; Length 422;

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LOCUS 4756 bp mRNA linear PRI 21-OCT-2000  
DEFINITION Homo sapiens Hu-Claspilin mRNA, complete cds.  
ACCESSION AF297866  
VERSION AF297866.1 GI:10944333  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 4756)  
AUTHORS Kumagai, A. and Dunphy, W.G.  
TITLE Claspilin, a novel protein required for the activation of Chk1 during  
a DNA replication checkpoint response in Xenopus egg extracts  
JOURNAL Mol. Cell 6 (4), 839-849 (2000)  
MEDLINE 21000493  
PUBMED 11090622  
REFERENCE 2 (bases 1 to 4756)  
AUTHORS Kumagai, A. and Dunphy, W.G.  
TITLE Direct Submission  
JOURNAL Submitted (21-AUG-2000) Biology, California Institute of  
Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA

FEATURES  
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Best Local Similarity 1.9%; Score 575; DB 9; Length 4756;

Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	55057	CGAGCTGCACCATTCGACATCCACCCTGGGTGAGAGAGCCAGACTCTGTCTCAAAAAA	55118
QY	14960	AAAAAAAAAAAAAGTTGTGATA -GTTAATAATAAAAAAGAGTACATTCGCTACTGTG	15018
Db	55117	AAAAAAAAAAAAAGTTGTGATAAGSTTAATATAAAAAGAGTACATTCGCTACTGTG	55176
QY	15019	TATGCTATTAGAATTTATTATTTCGCTTCCAACTCGAAATTAAGTTTTCTGTA	15078
Db	55177	TATGCTATTAGAATTTATTATTTCGCTTCCAACTCGAAATTAAGTTTTCTGTA	55233
QY	15079	ATCCGAGTCAAACTTAAGCATTGATGAAAACTCATTTACTTTTTACTGCTAAAG	15138
Db	55237	ATCCGAGTCAAACTTAAGCATTGATGAAAACTCATTTACTTTTTACTGCTAAAG	55299
QY	15139	GAACATTTTGCTCAGTTAAATTAATGTGMAACCGAATTTCTTTGTTTTCACATTT	15199
Db	55297	GAACATTTTGCTCAGTTAAATTAATGTGMAACCGAATTTCTTTGTTTTCACATTT	55355
QY	15199	CAACAATATTAAAGTATCTACTAGTAAAGTTGCTGTGGGCATACCAAGATAATCT	15258
Db	55357	CAACAATATTAAAGTATCTACTAGTAAAGTTGCTGTGGGCATACCAAGATAATCT	55416
QY	15259	GACATTTAAGTATACCTTAAGATGCTTTACTCTAATGGGCGGATTAAGAAATGCGAA	15318
Db	55417	GACATTTAAGTATACCTTAAGATGCTTTACTCTAATGGGCGGATTAAGAAATGCGAA	55478
QY	15319	TAAAGACTACAAAGAGAAATGCTAAATGATGCTTTGATTAATGAATATGCTATGATA	15378
Db	55477	TAAAGACTACAAAGAGAAATGCTAAATGATGCTTTGATTAATGAATATGCTATGATA	55533
QY	15379	ATTGGAAATTAATTAACATGAAGAAAAAGAAAGTATTTTCTTAAAGACATTAGAA	15438
Db	55537	ATTGGAAATTAATTAACATGAAGAAAAAGAAAGTATTTTCTTAAAGACATTAGAA	55599
QY	15439	AAAGTACTGGGAAATTCAGAGAAATTAATTTCTTCCAAATATGTTAAAGACAC	15499
Db	55597	AAAGTACTGGGAAATTCAGAGAAATTAATTTCTTCCAAATATGTTAAAGACAC	55656
QY	15499	CTGAAGATAGCTGATTAATTAATCTGTTCACTGCCCTTAACTAGTGAAGTGATA	15558
Db	55657	CTGAAGATAGCTGATTAATTAATCTGTTCACTGCCCTTAACTAGTGAAGTGATA	55716
QY	15559	TCTTCTGCTTGTTCCTACTCTATACCTTCCCTAGTCTCTCTCAGTGAGACACATTTGAG	15618
Db	55717	TCTTCTGCTTGTTCCTACTCTATACCTTCCCTAGTCTCTCTCAGTGAGACACATTTGAG	55776
QY	15619	CACCTGATTTATCAATGAATGAATGAAATATCCCTCAACACAGACTAAGTATTACACAT	15678
Db	55777	CACCTGATTTATCAATGAATGAATGAAATATCCCTCAACACAGACTAAGTATTACACAT	55836
QY	15679	TGAATTAATTTCCGACTCTTACATAGAGCTGATGCTCCCACTCTGCTTGAGGACAT	15738
Db	55837	TGAATTAATTTCCGACTCTTACATAGAGCTGATGCTCCCACTCTGCTTGAGGACAT	55896
QY	15739	ATGGAATGCTGTTAAGAGCTTAGACTTTGACCAAGACAGATTGGAATCTGAACATAG	15798
Db	55897	ATGGAATGCTGTTAAGAGCTTAGACTTTGACCAAGACAGATTGGAATCTGAACATAG	55956
QY	15799	CATGTAATTTGTTAAACATTTGATAGCCCATTTGACCTCTCAAGCATCTTTTGTTTAA	15858
Db	55957	CATGTAATTTGTTAAACATTTGATAGCCCATTTGACCTCTCAAGCATCTTTTGTTTAA	56016
QY	15859	AAAGAGAAGAAAGCCAGACACAGTGTGTGACACACTGTAGTTCCAGCTACCGAGCGTG	15918
Db	56017	AAAGAGAAGAAAGCCAGACACAGTGTGTGACACACTGTAGTTCCAGCTACCGAGCGTG	56076



D	49484	TGTCAGTAATCTTAATGCATCCCTTCAGGAACATTGTTGCTTCCTTAG	49543
Q	9381	TTACAGTTATATCCACGATGATTTGTGTCTATTAATCTACTTGGACCTTCGGTAC	9440
D	49544	TTACAGTTATATCCACGATGATTTGTGTCTATTAATCTACTTGGACCTTCGGTAC	49603
Q	9441	CTGCTGTGATATAAAGATATGTGATCTTCTAGTTGCTTCACTAGAAATCAATGACCA	9500
D	49604	CTGCTGTGATATAAAGATATGTGATCTTCTAGTTGCTTCACTAGAAATCAATGACCA	49663
Q	9501	AACGTATTTTCAAGAGAGAACAGATAGTCCCTGATAGTGGACAGGACGATGAA	9560
D	49664	AACGTATTTTCAAGAGAGAACAGATAGTCCCTGATAGTGGACAGGACGATGAA	49723
Q	9561	ACAATTTGACCTTGTAGTCAAGAGAGTTGTAATAGTACTTTTATTTTGGAAATAGTT	9620
D	49724	ACAATTTGACCTTGTAGTCAAGAGAGTTGTAATAGTACTTTTATTTTGGAAATAGTT	49783
Q	9621	GGGGAGCCTCAGTTGTAAGTATGATGATTAATTCATTAATCTTCTGATTTATTAAT	9680
D	49784	GGGGAGCCTCAGTTGTAAGTATGATGATTAATTCATTAATCTTCTGATTTATTAAT	49843
Q	9681	TATTAATGCCCATCTTATGTTGTTTATTAATTAAGCAAAATTAACAGTCTTGATAC	9740
D	49844	TATTAATGCCCATCTTATGTTGTTTATTAATTAAGCAAAATTAACAGTCTTGATAC	49903
Q	9741	CTTTTGAAGCTTATATGTTGTAATGCTTAATAGTACATACATATTCCTGTTAAT	9800
D	49904	CTTTTGAAGCTTATATGTTGTAATGCTTAATAGTACATACATATTCCTGTTAAT	49963
Q	9801	GCATTCATCTATTAATTAAGGAATTTTACACCTGGCGAGGTAGGAACAATTTTAC	9860
D	49964	GCATTCATCTATTAATTAAGGAATTTTACACCTGGCGAGGTAGGAACAATTTTAC	50023
Q	9861	ATTGTAATATACGTAATAATTTACATTTCCAGTAAGACATTTTCCACGAGAAATGT	9920
D	50024	ATTGTAATATACGTAATAATTTACATTTCCAGTAAGACATTTTCCACGAGAAATGT	50082
Q	9921	TTTTCAAAATGTAATTTAGATTTGCTTGTACATACAGTCTTAAACAGTACAGTA	9980
D	50083	TTTTCAAAATGTAATTTAGATTTGCTTGTACATACAGTCTTAAACAGTACAGTA	50142
Q	9981	ATTTCACAACTTATATATCATCTGTATTAATAATATTTTGGAGAGTATGGACTAG	10040
D	50143	ATTTCACAACTTATATATCATCTGTATTAATAATATTTTGGAGAGTATGGACTAG	50202
Q	10041	GAGGAAGATCAAAATGATGGTATTAATAAGCAAAATTTTCCCTCCAGATTCAGATGAG	10100
D	50203	GAGGAAGATCAAAATGATGGTATTAATAAGCAAAATTTTCCCTCCAGATTCAGATGAG	50262
Q	10101	AGATATTTTGAAGTAAGAGTTGAAAAACAGAAAGTTCTTCAAGACAGTATTCGAAA	10160
D	50263	AGATATTTTGAAGTAAGAGTTGAAAAACAGAAAGTTCTTCAAGACAGTATTCGAAA	50322
Q	10161	CAGAGGACAAAAAGCCTCTCCAGAGAAACTACTTATGACAGTGGCGAGAGGAAAAATA	10220
D	50323	CAGAGGACAAAAAGCCTCTCCAGAGAAACTACTTATGACAGTGGCGAGAGGAAAAATA	50382
Q	10221	AAGGAATTTATATCTGCGGAAAAATACAAAAATCAAAAGAGATTACAAAACTGTGCAG	10280
D	50383	AAGGAATTTATATCTGCGGAAAAATACAAAAATCAAAAGAGATTACAAAACTGTGCAG	50442
Q	10281	ACAGTATGAAAGTTACATGAGAAAGTCTTTGTATCAGAAAAATCTTGAAGCGCAAGTGA	10340
D	50443	ACAGTATGAAAGTTACATGAGAAAGTCTTTGTATCAGAAAAATCTTGAAGCGCAAGTGA	50502
Q	10341	AACCTTGCTTAGAGCTGAGTCTTCACTGGAACCTTACAGACTTACCAGTACAGAA	10400
D	50503	AACCTTGCTTAGAGCTGAGTCTTCACTGGAACCTTACAGACTTACCAGTACAGAA	50562
Q	10401	AGAGTTCCAAAAAGACATACATGATTAAGAGAACTGCAGAAAAAGCAAAAGTAAAT	10460
D	50563	AGAGTTCCAAAAAGACATACATGATTAAGAGAACTGCAGAAAAAGCAAAAGTAAAT	50622

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Q	10461	CAAAAAGAGACTTGAGAAAAAGAGAGAAAAATGAAAAATTTAGACGCTAAAAAGA	10520
D	50623	CAAAAAGAGACTTGAGAAAAAGAGAGAAAAATGAAAAATTTAGACGCTAAAAAGA	50682
Q	10521	AGAAAACAAAAAACAGGTACATTTTAAAGATATTTGCTATTTGCTGGGTAGGTTAAC	10580
D	50683	AGAAAACAAAAAACAGGTACATTTTAAAGATATTTGCTATTTGCTGGGTAGGTTAAC	50742
Q	10581	ATTTAGAAAAAGTTGCTGTTAGTACTTGAAGTTGTTTCTGCTCTGACATTTGCTTTG	10640
D	50743	ATTTAGAAAAAGTTGCTGTTAGTACTTGAAGTTGTTTCTGCTCTGACATTTGCTTTG	50802
Q	10641	AATGACATTTTGTGAGAAATTTATTCCTAATAGTATGATTTTAAACTAAGTGT	10700
D	50803	AATGACATTTTGTGAGAAATTTATTCCTAATAGTATGATTTTAAACTAAGTGT	50862
Q	10701	CTTGCCAGGTGACAGTGTGCTAATCCACAGACTTTGGAGGCTGAGGCCAGA	10760
D	50863	CTTGCCAGGTGACAGTGTGCTAATCCACAGACTTTGGAGGCTGAGGCCAGA	50922
Q	10761	GGGTCACTTAAGCCGAGAGTTCCAGAACAGCTTACGCAACAGAGTGAATCCATCT	10820
D	50923	GGGTCACTTAAGCCGAGAGTTCCAGAACAGCTTACGCAACAGAGTGAATCCATCT	50982
Q	10821	ACAAAAATTTAAATTAATGTTGGTGGTGGGCCGTAGTCCAGCTGTAGTCCAACTA	10880
D	50983	ACAAAAATTTAAATTAATGTTGGTGGTGGGCCGTAGTCCAGCTGTAGTCCAACTA	51042
Q	10881	CTTGGAGGTGAGGTGGGGAATCACTTGAAGCCAGAGAGTCAAGTCAATGAAGCT	10940
D	51043	CTTGGAGGTGAGGTGGGGAATCACTTGAAGCCAGAGAGTCAAGTCAATGAAGCT	51102
Q	10941	GTAATTCACACGCAATTCAGCTGATGACAGAGTGAAGCTGTCTCAAAAAAAA	11000
D	51103	GTAATTCACACGCAATTCAGCTGATGACAGAGTGAAGCTGTCTCAAAAAAAA	51162
Q	11001	AAAAACAAAAACCAAAAAACCAAACTATTGCTTATTTGTTGGTATGACAGAG	11060
D	51163	AAAAACAAAAACCAAAAAACCAAACTATTGCTTATTTGTTGGTATGACAGAG	51222
Q	11061	ACATTCGCAATTAATGGGTTTCTGATTTTCTTATGAGACATGAGTAATCTTGTCT	11120
D	51223	ACATTCGCAATTAATGGGTTTCTGATTTTCTTATGAGACATGAGTAATCTTGTCT	51282
Q	11121	GTCCTGAGCTGATGAATAATTAACAGAAAGGCTTTTATGCAATCTTCACTAGTA	11180
D	51283	GTCCTGAGCTGATGAATAATTAACAGAAAGGCTTTTATGCAATCTTCACTAGTA	51342
Q	11181	GTCCTGTTGCTAAGTGAATAAACATCTCAAAATTTATTAACAGTGTCTTAAACAATA	11240
D	51343	GTCCTGTTGCTAAGTGAATAAACATCTCAAAATTTATTAACAGTGTCTTAAACAATA	51402
Q	11241	TTTTACTTCAAAAAATTTACTGTTTATTAAGTATGTTTATGACAGTGTCAATAATC	11300
D	51403	TTTTACTTCAAAAAATTTACTGTTTATTAAGTATGTTTATGACAGTGTCAATAATC	51462
Q	11301	ACAACCTGCACTTCAAAAGATACATGATGATGAACACAGTAAGATGTTCTGATTTT	11360
D	51463	ACAACCTGCACTTCAAAAGATACATGATGATGAACACAGTAAGATGTTCTGATTTT	51522
Q	11361	ATATGCTGCTGTTGATGAACATGAGGCTTTTCTGGCTGATCCAAATTTGCATATGA	11420
D	51523	ATATGCTGCTGTTGATGAACATGAGGCTTTTCTGGCTGATCCAAATTTGCATATGA	51582
Q	11421	TGTTGGAATTAAGTATTTTAAAGATTTGATTTGTTTGTATGATTTACTTA	11480
D	51583	TGTTGGAATTAAGTATTTTAAAGATTTGATTTGTTTGTATGATTTACTTA	51642
Q	11481	GGAAGATGATGTGAACACGCAATTAATGACAGTGTCTCTCTGATTAAGAGCT	11540
D	51643	GGAAGATGATGTGAACACGCAATTAATGACAGTGTCTCTCTGATTAAGAGCT	51702

QY 7165 TACACACATAGTCTGAAGGTAAATTTATACAGCAATTTTAAATAATTTTCGTGCATGAGC 7224  
DB TACACACATAGTCTGAAGGTAAATTTATACAGCAATTTTAAATAATTTTCGTGCATGAGC 47383  
QY 7225 AAAGGTTTTACTGCGAGCTCATCATATGAGTTCAGGTGGAATTTTCATCTAGTGGCATC 7284  
DB AAAGGTTTTACTGCGAGCTCATCATATGAGTTCAGGTGGAATTTTCATCTAGTGGCATC 47443  
QY 7285 ATGTCAGTGTCAATATTTTGGAAATTTGGAGCAATTTTCAGATTTTCAGGTTAGAGATGTT 7344  
DB ATGTCAGTGTCAATATTTTGGAAATTTGGAGCAATTTTCAGATTTTCAGGTTAGAGATGTT 47503  
QY 7345 CAACCTGTATTTTCAAGTCATGCGCAATCTTGTATTCATACAGACTACCCATTTTCC 7404  
DB CAACCTGTATTTTCAAGTCATGCGCAATCTTGTATTCATACAGACTACCCATTTTCC 47563  
QY 7405 TCTCACAGGATTTATTTGCAAGAAATCCAGATATCATATTTTGAACACCAAGATTT 7464  
DB TCTCACAGGATTTATTTGCAAGAAATCCAGATATCATATTTTGAACACCAAGATTT 47623  
QY 7465 TAGTGTGCATATCTAACAACAAGAGCTTTTCCAAAAATAGATACATATTTATTACCA 7524  
DB TAGTGTGCATATCTAACAACAAGAGCTTTTCCAAAAATAGATACATATTTATTACCA 47683  
QY 7525 CACCTAAGAAGTATCTAGTCAGTGTTCAGATTTCTTTGACTCAGAGATATTTCAATTTAT 7584  
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QY 7585 TTTATATGCCACTTTAGCATATTTATTTACATTTTACATTTTGTATTTTGAATCATCATCCGAG 7644  
DB TTTATATGCCACTTTAGCATATTTATTTACATTTTGTATTTTGAATCATCATCCGAG 47803  
QY 7645 TTGCGATTTTGTAAATTTTATATATATATGATATATGATATATGATATTTATTT 7704  
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QY 7705 AAGATATACATATATATAAGCATACATTTTATGATATATAGAAATATACAGGGCCGGTT 7764  
DB AAGATATACATATATAAGCATACATTTTATGATATATAGAAATATACAGGGCCGGTT 47923  
QY 7765 GTGGTGGCTTACCTGTATTTCCAGCATTTTGGGAGGCTGAGGCGGATCACTCA 7824  
DB GTGGTGGCTTACCTGTATTTCCAGCATTTTGGGAGGCTGAGGCGGATCACTCA 47983  
QY 7825 GGTCAAAAGTTCCAGACCACTGCTTAACATTTGTCAAACCCGTTTCTACAAAAATTA 7884  
DB GGTCAAAAGTTCCAGACCACTGCTTAACATTTGTCAAACCCGTTTCTACAAAAATTA 48043  
QY 7885 GCCGGCATGGTGGCAGCAGCTGTAAATCCAGCTACTCGGAGGCTGAGGCTGGAGAT 7944  
DB GCCGGCATGGTGGCAGCAGCTGTAAATCCAGCTACTCGGAGGCTGAGGCTGGAGAT 48103  
QY 7945 CCCTTCAACCCAGGAGGCGGAGTTGAGGAGCCCAAGATCGTGCCATTTGCACCTCAGCT 8004  
DB CCCTTCAACCCAGGAGGCGGAGTTGAGGAGCCCAAGATCGTGCCATTTGCACCTCAGCT 48163  
QY 8005 TGGCCAAATAAGAGCAAACTCCGCTCAAAAAAGAAAAAGAAATATACATATAGCGG 8064  
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QY 8065 GCGGTGGTGGCTCAGCTGTATTTCCACCACTTTGGGAGGCTGAGGCGGCGATCACC 8124  
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QY 8125 TCAGGTCCAGAGTTGGAGACCAAGCTGACTTAACATGGAGAAACCCCATCTCTACTAAAAA 8184  
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QY 8185 TACAAAATTTAGCAGACGTTGGTACACATGCTGTATTTCCAGCTACTTCGGGAGGCTGAG 8244  
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DB GCAGGAGATCGCTTTGAACCTGGGAGGAGGTTGCGGTGAGCGGAGATCGCGCGGTTG 48404  
QY 8305 CGCTCCATCTCGGGCGACAAACGCAACCTCCATCTCAAAAAAGAAATATACACATA 8364  
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QY 8425 ATACATTCATTTATGTTTAACTTTCTTTATAGGTTTCTCTCCCTCTCTTTTTTTTCT 8484  
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QY 8485 TTCCAATATATTTTAAAGAAACCGCGGTCAGTGGCTGATGCTGCTATACCTGTAATCCAGCA 8544  
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QY 8605 GCATGTGAACCTTCTCTTATTAATAAGAAATTTAGCTGGGTGTTGATGTCG 8664  
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QY 8665 CCGTGAATCCCAGCTACTCAGGAGGCTGAGGAGGATCGCTTCAACCCAGGAGGAG 8724  
DB CCGTGAATCCCAGCTACTCAGGAGGCTGAGGAGGATCGCTTCAACCCAGGAGGAG 48883  
QY 8725 AGTTCAGTGGAGGAGGATTCGACCACTGCACTCCAGCTGGGTGACAGCGAGATTC 8784  
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QY 8785 TATCTCAAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8840  
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QY 8841 ACTTGTAGATTTTCCAGCTCTAGATTCGATATCTGTGTATTTTATCAACATGTTCCCT 8900  
DB ACTTGTAGATTTTCCAGCTCTAGATTCGATATCTGTGTATTTTATCAACATGTTCCCT 49063  
QY 8901 ATTCCTCTATTTCTTATAAATTCGATCTAGATCTAGAGCTTGTATGATTTCAAAATTT 8960  
DB ATTCCTCTATTTCTTATAAATTCGATCTAGATCTAGAGCTTGTATGATTTCAAAATTT 49123  
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QY 9201 GTTCACAGAGAAAGGATATAAATGCTGATTTCTTTTCAATTTTTTTTTTACCGTTAC 9260  
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QY 9261 TAAAGAGTTGGTCTGTTAGCATCTTCAAGGTGAAATGAACHTTTTGTGTTGTTGT 9320  
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QY 6625 CCAAGCTAGTCTGCAACTCTGAGCTTGTGATCCAGCCAGCTCCGAGCTCCCAAGTCTG 6684  
Db 46784 CCAAGCTAGTCTGCAACTCTGAGCTTGTGATCCAGCCAGCTCCGAGCTCCCAAGTCTG 46843  
QY 6685 GATATCAGCGCTGAGCGACCATGCTGACCAATTTATTAATTTTGAAGAAACCTCA 6744  
Db 46844 GATATCAGCGCTGAGCGACCATGCTGACCAATTTATTAATTTTGAAGAAACCTCA 46903  
QY 6745 GCTGAGGCTTGTGGCCCTGTATATTTAGATTTGATTTGATTTGATTTGATTTGAT 6804  
Db 46904 GCTGAGGCTTGTGGCCCTGTATATTTAGATTTGATTTGATTTGATTTGATTTGAT 46963  
QY 6805 TGAATCAGACCCCTGAGAACACTAAGAGATAGACTTGGCATCTAGGGTTACTTTAAG 6864  
Db 46964 TGAATCAGACCCCTGAGAACACTAAGAGATAGACTTGGCATCTAGGGTTACTTTAAG 47023  
QY 6865 TCATCAATGATCAATGATCAATCAACACCCCTCTCTAGGTTTATTTGCGACCTT 6924  
Db 47024 TCATCAATGATCAATGATCAATCAACACCCCTCTCTAGGTTTATTTGCGACCTT 47083  
QY 6925 TTAATCTGCTTATTTAGAAATTTTCAACGCTATCAACCGTAGAAAGGATGTTAATG 6984  
Db 47084 TTAATCTGCTTATTTAGAAATTTTCAACGCTATCAACCGTAGAAAGGATGTTAATG 47143  
QY 6985 AACCATCACTTACTTCACTCACTAAGTTGAATCTCGTCAAAATGCTTGGAGCA 7044  
Db 47144 AACCATCACTTACTTCACTCACTAAGTTGAATCTCGTCAAAATGCTTGGAGCA 47203  
QY 7045 GAAAGCTTTGAAATTTCAATTTGATTTGATTTGGAATTTGCAATACATTAATGAG 7104  
Db 47204 GAAAGCTTTGAAATTTCAATTTGATTTGGAATTTGCAATACATTAATGAG 47263  
QY 7105 ATATCTTGGGAGGAGCCAGTCTAAACATGAATTCAGTATATTTCAATATATCT 7164  
Db 47264 ATATCTTGGGAGGAGCCAGTCTAAACATGAATTCAGTATATTTCAATATATCT 47323









[illegible]



[illegible]

Oy	19021	GAGCTGTGATCGACCCAGCTGACATCCAGCTTGAGCAAGACAGACACCTGTCTTAA	19080
Db	58468	GAGCTGTGATCGACCCAGCTGACATCCAGCTTGAGCAAGACAGACACCTGTCTTAA	58527
Oy	19081	AAGACAATGAAAAAGTGGCTGGGACAAATGGCTGACACCTGTAACTTGGCACTTTGGGA	19140
Db	58528	AAGACAATGAAAAAGTGGCTGGGACAAATGGCTGACACCTGTAACTTGGCACTTTGGGA	58587
Oy	19141	GGCTGAGGAGGATGATCATTTCAATGTCAGAGAGTTCAAGACAGCTGGACAACATGGCA	19200
Db	58588	GGCTGAGGAGGATGATCATTTCAATGTCAGAGAGTTCAAGACAGCTGGACAACATGGCA	58647
Oy	19201	AAACCGGTCTCTACAAAAAATACAAAAATCGGCAATCGGCAATCGGCTGCTCTCTATTC	19260
Db	58648	AAACCGGTCTCTACAAAAAATACAAAAATCGGCAATCGGCAATCGGCTGCTCTCTATTC	58707
Oy	19261	TCAGCACTTTGGAGGCGCAGAGTGGGTGATCATGAGATCAGAGAGTTCAAGACAGCC	19320
Db	58708	TCAGCACTTTGGAGGCGCAGAGTGGGTGATCATGAGATCAGAGAGTTCAAGACAGCC	58767
Oy	19321	TGGCCAAATGATGAAAAACCCCATCTTACTAAAAATAAAAATAAAAATTAAGCTGGGTG	19380
Db	58768	TGGCCAAATGATGAAAAACCCCATCTTACTAAAAATAAAAATAAAAATTAAGCTGGGTG	58827
Oy	19381	TGCTGACGATGCTCTTAATCCAGCTTGTAGAGAGGCTGAGGAGGAAATTCCTTGA	19440
Db	58828	TGCTGACGATGCTCTTAATCCAGCTTGTAGAGAGGCTGAGGAGGAAATTCCTTGA	58887
Oy	19441	CCCAGAGGTGAGGTTTACAGTGAAGCCGAGATCATCCACTGCTTTGGCTGGGCAAC	19500
Db	58888	CCCAGAGGTGAGGTTTACAGTGAAGCCGAGATCATCCACTGCTTTGGCTGGGCAAC	58947
Oy	19501	AAGAGTAGACTCCGCTCTCAAAAAAATTAAGTGGATATGCTGGTACATGC	19560
Db	58948	AAGAGTAGACTCCGCTCTCAAAAAAATTAAGTGGATATGCTGGTACATGC	59007
Oy	19561	CTATAGTCTGGCTATCTCAGAGGCTGAGTGAAGATCACTTAAGCTGGGGAGA	19620
Db	59008	CTATAGTCTGGCTATCTCAGAGGCTGAGTGAAGATCACTTAAGCTGGGGAGA	59067
Oy	19621	TTGAGGCTACAGTGAAGGCAAGATTGCAACCACTGCTCAAGCTGGGCGCAAAAGCGA	19680
Db	59068	TTGAGGCTACAGTGAAGGCAAGATTGCAACCACTGCTCAAGCTGGGCGCAAAAGCGA	59127
Oy	19681	GACTCATTTAAAAAATTAACCATTTTATCATGAGAGAGAGGCGCTGAAATATTCAG	19740
Db	59128	GACTCATTTAAAAAATTAACCATTTTATCATGAGAGAGAGGCGCTGAAATATTCAG	59187
Oy	19741	TGTGATCACTCCAAAGAACTTTCTCCTTAAAACTGCCAGCTCTCATCAAGATTCCA	19800
Db	59188	TGTGATCACTCCAAAGAACTTTCTCCTTAAAACTGCCAGCTCTCATCAAGATTCCA	59247
Oy	19801	TTATGATATGAAGTTTAAAGATATTGCACTGGGGAAGAGGCTTAAGTTATATCATATG	19860
Db	59248	TTATGATATGAAGTTTAAAGATATTGCACTGGGGAAGAGGCTTAAGTTATATCATATG	59307
Oy	19861	GGGAGAGAAATTTAAGATATTGCACTGGGGAAGAGGCTTAAGTTATATCATATG	19920
Db	59308	GGGAGAGAAATTTAAGATATTGCACTGGGGAAGAGGCTTAAGTTATATCATATG	59367
Oy	19921	GATTGCTCACTCTGTTGCCATATATATATTTCCGTTTGTATACAAGTTGACAT	19980
Db	59368	GATTGCTCACTCTGTTGCCATATATATATTTCCGTTTGTATACAAGTTGACAT	59427
Oy	19981	GTGCTACTGGGCTGACATATTTCTTCTCATGTGACCAATGTACTAGAGTAAGTT	20040
Db	59428	GTGCTACTGGGCTGACATATTTCTTCTCATGTGACCAATGTACTAGAGTAAGTT	59487
Oy	20041	TTTCAAAAAAATTTTACAGTCTGCTGCTTATGTTATATCACTGAGCTGATTCAT	20100
Db	59488	TTTCAAAAAAATTTTACAGTCTGCTGCTTATGTTATATCACTGAGCTGATTCAT	59547
Oy	20101	TTATTTCCCTTTTGAAAAAATTTGACTTGCCTATATTTAGTAACATTCGCAATATG	20160

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Db	59548	TTATTTCCCTTTTGAAAAAATTTGACTTGCCTATATTTAGTAACATTCGCAATATG	59607
Oy	20161	AAACATTCAAAAATAGGAATTTGATCCAGCATTTTGGAGGCGCAAGTGGGCTGATCAT	20220
Db	59608	AAACATTCAAAAATAGGAATTTGATCCAGCATTTTGGAGGCGCAAGTGGGCTGATCAT	59667
Oy	20221	TTGAGGTGAGAGTTTCCAGACACAGCTTGGCTAACATGCTGAACCTGTCTCTTAA	20280
Db	59668	TTGAGGTGAGAGTTTCCAGACACAGCTTGGCTAACATGCTGAACCTGTCTCTTAA	59727
Oy	20281	ATACAAAAAATTAAGCTGGGCAATAGAGTGAAGTGTCTCACTGTAACTCTACTAGAGAC	20340
Db	59728	ATACAAAAAATTAAGCTGGGCAATAGAGTGAAGTGTCTCACTGTAACTCTACTAGAGAC	59787
Oy	20341	TGAGGAGAGATTCCTGTTGAACCTTGAGATGAGAGTTGCACTGAGCTGAGATCATC	20400
Db	59788	TGAGGAGAGATTCCTGTTGAACCTTGAGATGAGAGTTGCACTGAGCTGAGATCATC	59847
Oy	20401	ACTGCACTCCAGCTGGGCAATAGAGTGAAGTGTCTCACTGTAACTCTACTAGAGAC	20460
Db	59848	ACTGCACTCCAGCTGGGCAATAGAGTGAAGTGTCTCACTGTAACTCTACTAGAGAC	59907
Oy	20461	CAATACAAATAGGAAATTTTAAAGAGACCAAAACCCATGAAAAATTAAGCCCTTGA	20520
Db	59908	CAATACAAATAGGAAATTTTAAAGAGACCAAAACCCATGAAAAATTAAGCCCTTGA	59967
Oy	20521	TGATGAGATTAATATCTTTTCTTCTCACTGTTAATTAATTTTAAAGAAATTTTAA	20580
Db	59968	TGATGAGATTAATATCTTTTCTTCTCACTGTTAATTAATTTTAAAGAAATTTTAA	60027
Oy	20581	TGTTCAAAAGATTCGACATATTTAGAAATTTAGATTAATTTTCTGCTGATTTTAA	20640
Db	60028	TGTTCAAAAGATTCGACATATTTAGAAATTTAGATTAATTTTCTGCTGATTTTAA	60087
Oy	20641	AAGTCTATTTTGAACCTTGAGAAAGAACAGTGTGSCAGTCAATTAGTTGGTTAA	20700
Db	60088	AAGTCTATTTTGAACCTTGAGAAAGAACAGTGTGSCAGTCAATTAGTTGGTTAA	60147
Oy	20701	GTTGTATGAATTTGACACAGAGTGTAGTACAAAGGGTTTTGGTTCTCTGATATG	20760
Db	60148	GTTGTATGAATTTGACACAGAGTGTAGTACAAAGGGTTTTGGTTCTCTGATATG	60207
Oy	20761	TGCTTCCCTCATATTTGTTGAGCTAAAAAATTAAGTTATTAAGTAAAGAAAGA	20820
Db	60208	TGCTTCCCTCATATTTGTTGAGCTAAAAAATTAAGTTATTAAGTAAAGAAAGA	60267
Oy	20821	GTTTGTGACATGGCAAACTGACACAGTGTGGCTTTGGCTTTAGAACTGCAAGCTTG	20880
Db	60268	GTTTGTGACATGGCAAACTGACACAGTGTGGCTTTGGCTTTAGAACTGCAAGCTTG	60327
Oy	20881	AAGCAGGTTTTGGAAGCATGCTAATCCAGCAGCCAAACCCAGGCTGTCAGACAGTG	20940
Db	60328	AAGCAGGTTTTGGAAGCATGCTAATCCAGCAGCCAAACCCAGGCTGTCAGACAGTG	60387
Oy	20941	AATGTAGCTCATATGTAAGAAACATGGGCACTGATGAGAAAGAGAGCTAAAGCAGAT	21000
Db	60388	AATGTAGCTCATATGTAAGAAACATGGGCACTGATGAGAAAGAGAGCTAAAGCAGAT	60447
Oy	21001	GTGCTACTGCTGACTTACAGCACTTAAGAAAGTTGATGAGAGCAAGCCACAAACAGAT	21060
Db	60448	GTGCTACTGCTGACTTACAGCACTTAAGAAAGTTGATGAGAGCAAGCCACAAACAGAT	60507
Oy	21061	ATTGAGCCCAAGGTTTTGTTTTGCTTTTGTATTTCAATCAAGATCTTCAAGG	21120
Db	60508	ATTGAGCCCAAGGTTTTGTTTTGCTTTTGTATTTCAATCAAGATCTTCAAGG	60567
Oy	21121	CTATGAAAAAATTTATGAAAAAGTTATAGAAATCTTTTCTTGAGAGCTTTCAGAGC	21180
Db	60568	CTATGAAAAAATTTATGAAAAAGTTATAGAAATCTTTTCTTGAGAGCTTTCAGAGC	60627
Oy	21181	AGTATCTGCGCATGATTCAGGTAGCACTTGAAGCTGTGGGTGAGCAAGCTGGCT	21240



OY 14641 ATCTAACCATGTTTAAATGGAAGTCTGTTGGCTGGGTGCTTACGCCGTGAAT 14700  
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DB 54268 AGCATCTGTAGTCTTACAGTACTACGAGAGCTGGGCGAGAGAAATTAAGTGAACCCAGAA 54327  
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OY 15781 GATTTGAATCTTAATACATAGTAATTTTAACTATGTTATAGCCATTTGACCTCTTC 15840  
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DB 55588 ACTTTTTTTTTTGAAGAGGCTTCACTTCTCTCCCACTAGCTGAGAGTGCATGTC 55647  
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OY 16201 TGGCATCTCGGCTACAGCAACCTCCGCTCTCTGCTTCAAGCAATCTTCTGCTCAGG 16260  
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OY 16261 CTCTCAAGTACGCTGGATATACAGTACCCGCAACACACAGCTAATTTTGTATTTT 16320  
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DB 56068 AAAAAAAAAACAAAAAATTAATCTTTCAATTAACATCTTATGTTGGAGAGTGTATGT 56127  
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DB 56128 CACTGACTATCTGCTGCTGTAATAATGCTGAGTACGCTGTAATGAATGGCTGAC 56187  
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Db	51868	TAGTCACACTGATCTCTTTACACAGGAGATATAGATTCTTAGGGATAAATATTTATT	51927	QY	13561	ACAGTATATATATTTGCTTGTATTTATTCATTTTATAGAGTCTGCACCTGAACCTTCCATA	13620
QY	12481	TTGCTATCATATTTTCTGTTACCCATCATATTTGCTTTGACATAGTACGACAAATA	12540	Db	53008	ACAGTATATATATTTGCTTGTATTTATTCATTTTATAGAGTCTGCACCTGAACCTTCCATA	53067
Db	51928	TTGCTATCATATTTTCTGTTACCCATCATATTTGCTTTGACATAGTACGACAAATA	51987	QY	13621	TCATATGCCTGAGAAATAAACCAATTCATGATTTCTTCAACGTAACCCGGGCCACTTG	13680
QY	12541	TGGATTGGATTGAACAAATTTCTCTGAGACTTGGGAATAAATGAATTCCTTGAAGTTATAC	12600	Db	53068	TCATATGCCTGAGAAATAAACCAATTCATGATTTCTTCAACGTAACCCGGGCCACTTG	53127
Db	51988	TGGATTGGATTGAACAAATTTCTCTGAGACTTGGGAATAAATGAATTCCTTGAAGTTATAC	52047	QY	13681	CCACGAAATGCCATGGCACTATTGAAGTAAGAACCTCTTCTTCTTATATATATTTTCAT	13740
QY	12601	TGCATTTGGGCTTACTCATCTACTATTTCCTTCTCTCTTCTTCTGAGAGAGCAACT	12660	Db	53128	CCACGAAATGCCATGGCACTATTGAAGTAAGAACCTCTTCTTCTTATATATATTTTCAT	53187
Db	52048	TGCATTTGGGCTTACTCATCTACTATTTCCTTCTCTCTTCTTCTGAGAGAGCAACT	52107	QY	13741	GAACATTTAGTTTGTAGCAACATCTGGCATAAAAAGTTTCAGATTTCTCACTCCCTTAA	13800
QY	12661	CTTGAGTGATGAATATCTATCTTCTTGATATTCATATAATTAATGTAGTCTCACTTCTT	12720	Db	53188	GAACATTTAGTTTGTAGCAACATCTGGCATAAAAAGTTTCAGATTTCTCACTCCCTTAA	53247
Db	52108	CTTGAGTGATGAATATCTATCTTCTTGATATTCATATAATTAATGTAGTCTCACTTCTT	52167	QY	13801	AACTGATTTAACTGATATATCTAAGGGATGAGATGTTTCACATTTAGGATTAATTTTCA	13860
QY	12721	GTTTCTTTAAGGAAAGAAAGGAGCCAGATTAAGTAAGAACGATTAACCAACTGCAAT	12780	Db	53248	AACTGATTTAACTGATATATCTAAGGGATGAGATGTTTCACATTTAGGATTAATTTTCA	53307
Db	52168	GTTTCTTTAAGGAAAGAAAGGAGCCAGATTAAGTAAGAACGATTAACCAACTGCAAT	52227	QY	13861	ACTCCAGCTCAATTTCTCTCTCTAGSTCATCTAATATATCAGTCAAGCCATCACAAGAA	13920
QY	12781	AGTCAGACTCAGGCGCTTATTTCGAGGTAAATGCAACCCAGTAAACTTTGAGGCAAAATCAC	12840	Db	53308	ACTCCAGCTCAATTTCTCTCTCTAGSTCATCTAATATATCAGTCAAGCCATCACAAGAA	53367
Db	52228	AGTCAGACTCAGGCGCTTATTTCGAGGTAAATGCAACCCAGTAAACTTTGAGGCAAAATCAC	52287	QY	13921	ATCATAGACACTGCAAAATCTACTGAAATGAACAGTGTACCATAGTAAAGTTCTGAG	13980
QY	12841	AACATTTCTTTGAGCTCAACTTGGATGTTGGGACTTTTATTTTAACTTTCTAA	12900	Db	53368	ATCATAGACACTGCAAAATCTACTGAAATGAACAGTGTACCATAGTAAAGTTCTGAG	53427
Db	52288	AACATTTCTTTGAGCTCAACTTGGATGTTGGGACTTTTATTTTAACTTTCTAA	52347	QY	13981	CAGCAACAGGTGCAAAATGAAGTGGAACTTAATGCACTCCCTGTAGTTTCAAGGAA	14040
QY	12901	TGTGAACACTCAGGTTAATTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAG	12960	Db	53428	CAGCAACAGGTGCAAAATGAAGTGGAACTTAATGCACTCCCTGTAGTTTCAAGGAA	53487
Db	52348	TGTGAACACTCAGGTTAATTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAG	52407	QY	14041	ACCCAGATCATTTACTTGGATCAGATGAGTCTTTCAGGAAGGATTTGGTAAAAAATCAAG	14100
QY	12961	AAGCCCTTGAACATTAGTATAAATTTTCAAGACTGTAGTGCAGGTAAAGCA	13020	Db	53488	ACCCAGATCATTTACTTGGATCAGATGAGTCTTTCAGGAAGGATTTGGTAAAAAATCAAG	53547
Db	52408	AAGCCCTTGAACATTAGTATAAATTTTCAAGACTGTAGTGCAGGTAAAGCA	52467	QY	14101	CTAGAAATTCAGGAGAAACAGAGAGTGTACATTTAGACCTTACCTGGGGACAGCTCA	14160
QY	13021	GGAAATTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTT	13080	Db	53548	CTAGAAATTCAGGAGAAACAGAGAGTGTACATTTAGACCTTACCTGGGGACAGCTCA	53607
Db	52468	GGAAATTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTT	52527	QY	14161	GTGTTGCAACAGGAATCCAACTTCTCGGGAACAAATCAGTGAAGAAATGTGAGGTGGA	14220
QY	13081	ATCCCTCCCTTATTTGAGTTTGGTTACCTGTGTCAGCCATGTCAGGAACTTAAXAA	13140	Db	53608	GTGTTGCAACAGGAATCCAACTTCTCGGGAACAAATCAGTGAAGAAATGTGAGGTGGA	53667
Db	52528	ATCCCTCCCTTATTTGAGTTTGGTTACCTGTGTCAGCCATGTCAGGAACTTAAXAA	52587	QY	14221	GGGCTTGTAGCATTTGAACCTCATGCCCTGGAGGGTGAAGGCCCCCAAAATCCAGAAGA	14280
QY	13141	TATCATCCCTTGTCCAGAGTATCAGCTGTATACATTAACCTGCCTGTAGTCCGTAGT	13200	Db	53668	GGGCTTGTAGCATTTGAACCTCATGCCCTGGAGGGTGAAGGCCCCCAAAATCCAGAAGA	53727
Db	52588	TATCATCCCTTGTCCAGAGTATCAGCTGTATACATTAACCTGCCTGTAGTCCGTAGT	52647	QY	14281	ACAGATGAGAAAGTGAAGAGCCTGAGCAGCAAAATAATCATCAGCAGTTGGGCCACCT	14340
QY	13201	AGCCCTCTCAGTTATCAGATCAAAACACACTGCATGTTTGTAGTACCATCTGCAGTTCA	13260	Db	53728	ACAGATGAGAAAGTGAAGAGCCTGAGCAGCAAAATAATCATCAGCAGTTGGGCCACCT	53787
Db	52648	AGCCCTCTCAGTTATCAGATCAAAACACACTGCATGTTTGTAGTACCATCTGCAGTTCA	52707	QY	14341	GAATAAGTGAGAGGTTTACTCTGGATAGACTTAAGCAACTGGGAGTAGATTTCCATT	14400
QY	13261	GGCATCCACTGCAGGTTTGGAAATGTCTGTCTGGATAAGGGGGAGTACTGTATATAA	13320	Db	53788	GAATAAGTGAGAGGTTTACTCTGGATAGACTTAAGCAACTGGGAGTAGATTTCCATT	53847
Db	52708	GGCATCCACTGCAGGTTTGGAAATGTCTGTCTGGATAAGGGGGAGTACTGTATATAA	52767	QY	14401	AAACACCGCTAGGTGCTGATGAAGATTTCTTGTGATACCTTGAACCTGAAACCAAGA	14460
QY	13321	ATGTTTAGTCCCAAGAGATTTCTGATTCAGTAGATTCGAATGGATCCCAAGATCTGT	13380	Db	53848	AAACACCGCTAGGTGCTGATGAAGATTTCTTGTGATACCTTGAACCTGAAACCAAGA	53907
Db	52768	ATGTTTAGTCCCAAGAGATTTCTGATTCAGTAGATTCGAATGGATCCCAAGATCTGT	52827	QY	14461	GGTAAATCCTTTACATTTGTGGGAGCCTCCCTGGAGTGATTTATCTGGTAGCTTTTGATTA	14520
QY	13381	ATTTCTAAAAAATCTTCTGGATCATTTTGTATTTACATCTAGTTTAAAGCCACTGTCT	13440	Db	53908	GGTAAATCCTTTACATTTGTGGGAGCCTCCCTGGAGTGATTTATCTGGTAGCTTTTGATTA	53967
Db	52828	ATTTCTAAAAAATCTTCTGGATCATTTTGTATTTACATCTAGTTTAAAGCCACTGTCT	52887	QY	14521	TTGACTACTGTCAGGAGACAGAAACACAGGAGGAAACCAATTAACCACTTTGATCTTATCCT	14580
QY	13441	TTGAGGAGCTTTTGTACTTAGCTCCTCTGCTCTTGTAAAGGGGAGTTTCTTATTTTC	13500	Db	53968	TTGACTACTGTCAGGAGACAGAAACACAGGAGGAAACCAATTAACCACTTTGATCTTATCCT	54027
Db	52888	TTGAGGAGCTTTTGTACTTAGCTCCTCTGCTCTTGTAAAGGGGAGTTTCTTATTTTC	52947	QY	14581	GCAGTTGTCAGATATGGGCAGAGTCTTTTATAGAAATTTTGGCAGGGGTATCAGAAATG	14640
QY	13501	TAGTCATGGCTTTGGTTATTTAGTTTAACTGAATATGAAGTGACATTTTCAAGATAT	13560	Db	54028	GCAGTTGTCAGATATGGGCAGAGTCTTTTATAGAAATTTTGGCAGGGGTATCAGAAATG	54087
Db	52948	TAGTCATGGCTTTGGTTATTTAGTTTAACTGAATATGAAGTGACATTTTCAAGATAT	53007				



QY	10261	GATTTCACAACTGTGGCAGACAGTATGAAGTACATGCAAAAGCTCTTTGTATCAGGA	10320		
Db	49708	GATTTCACAAAGTGTGGCAGACAGTATGAAGTACATGCAAAAGCTCTTTGTATCAGGA	49767		
QY	10321	AAATCTGAAGGCAAGTGAAGAACTGCTTGAAGCTGAGTCTTCACTGGAAGCTCTAC	10380		
Db	49768	AAATCTGAAGGCAAGTGAAGAACTGCTTGAAGCTGAGTCTTCACTGGAAGCTCTAC	49827		
QY	10381	AGACTTACACAGTACAGAAAGAGTTCACAAAGAGCATATGATTAAGAAAGAACTAC	10440		
Db	49828	AGACTTACACAGTACAGAAAGAGTTCACAAAGAGCATATGATTAAGAAAGAACTAC	49887		
QY	10441	AGGAAAGGCAAGTGAAGTGAAGAAAGAGCTTGAAGAAAGAGAGAGAAAGTGAAGAA	10500		
Db	49888	AGGAAAGGCAAGTGAAGTGAAGAAAGAGCTTGAAGAAAGAGAGAGAAAGTGAAGAA	49947		
QY	10501	AATTAAGACAGTAAAGAAAGAGAAAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG	10560		
Db	49948	AATTAAGACAGTAAAGAAAGAGAAAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG	50007		
QY	10561	TATTCCTTGGGTAAGTGAAGTGAAGAAAGTGTGCTGATGATGATGATGATGATGAT	10620		
Db	50008	TATTCCTTGGGTAAGTGAAGTGAAGAAAGTGTGCTGATGATGATGATGATGATGAT	50067		
QY	10621	GCTCTGACATATTCCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT	10680		
Db	50068	GCTCTGACATATTCCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT	50127		
QY	10681	GTGATTTAAACTAAGTGTGCTTGGCCAGGTGATGATGATGATGATGATGATGATGAT	10740		
Db	50128	GTGATTTAAACTAAGTGTGCTTGGCCAGGTGATGATGATGATGATGATGATGATGAT	50187		
QY	10741	TTTGGAGGCTGAGGCGCAGAGGCTGATTAAGCCAGAGTTCGAGAACAGCTAGGCA	10800		
Db	50188	TTTGGAGGCTGAGGCGCAGAGGCTGATTAAGCCAGAGTTCGAGAACAGCTAGGCA	50247		
QY	10801	CAGACTGAGATCCCATCTCTCAAAAAAATTTAAATTAATGTTGGTGTGGGCTGCTGT	10860		
Db	50248	CAGACTGAGATCCCATCTCTCAAAAAAATTTAAATTAATGTTGGTGTGGGCTGCTGT	50307		
QY	10861	CCGAGCTGATCCCATCTCTCTGAGAGGCTGAGGCTGAGAGATCTGAGAGGCTGAGAA	10920		
Db	50308	CCGAGCTGATCCCATCTCTCTGAGAGGCTGAGGCTGAGAGATCTGAGAGGCTGAGAA	50367		
QY	10921	GTCGAGGCTGCAATGAAGCTGTAATGTGACACAGTCACTGAGCTGATGACAGAGTGA	10980		
Db	50368	GTCGAGGCTGCAATGAAGCTGTAATGTGACACAGTCACTGAGCTGATGACAGAGTGA	50427		
QY	10981	GACCTGTCTCAAAAAAAGCAAAAAACCAAAACCTTATGCTTATTT	11040		
Db	50428	GACCTGTCTCAAAAAAAGCAAAAAACCAAAACCTTATGCTTATTT	50487		
QY	11041	CTATTTGGGATGACAGAGCATTTCCAAATTAATGCTTCTGATTTCTTTATGAGC	11100		
Db	50488	CTATTTGGGATGACAGAGCATTTCCAAATTAATGCTTCTGATTTCTTTATGAGC	50547		
QY	11101	ACATGAGTAAATCTTCTGCTCTCTGAGCTGATGAATAATTAATGAAAGAGCTTTT	11160		
Db	50548	ACATGAGTAAATCTTCTGCTCTCTGAGCTGATGAATAATTAATGAAAGAGCTTTT	50607		
QY	11161	TATGATCTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	11220		
Db	50608	TATGATCTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	50667		
QY	11221	AATAGTGTGCTTAACAGATATTTACTCAAAAAAATTTAGCTTATTAAGTTAGT	11280		
Db	50668	AATAGTGTGCTTAACAGATATTTACTCAAAAAAATTTAGCTTATTAAGTTAGT	50727		
QY	11281	TTAGACAGTGTGATTAACAACTTGACCTCAAAAGATGATGATGATGATGATGATGAT	11340		
Db	50728	TTAGACAGTGTGATTAACAACTTGACCTCAAAAGATGATGATGATGATGATGATGAT	50787		
QY	11341	GTAAGATGTTCTAGATTTATATGCTTGTCTGTGATGAACATGGGCTTTTCTGGCC	11400		
Db	50788	GTAAGATGTTCTAGATTTATATGCTTGTCTGTGATGAACATGGGCTTTTCTGGCC	50847		
QY	11401	TCATCAAAATGGCCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT	11460		
Db	50848	TCATCAAAATGGCCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT	50907		
QY	11461	TTTTCTTTATGATTTACTAGGAAAGATGATGATGATGATGATGATGATGATGATGAT	11520		
Db	50908	TTTTCTTTATGATTTACTAGGAAAGATGATGATGATGATGATGATGATGATGATGAT	50967		
QY	11521	CTCTTGGGATTAAGAGACCTTTTGAAGTGTGCTGAGATGAAATTAACCTCCATTC	11580		
Db	50968	CTCTTGGGATTAAGAGACCTTTTGAAGTGTGCTGAGATGAAATTAACCTCCATTC	51027		
QY	11581	GAGATGAAGATCATTAAGATCAATTAAGACAGCTGTAAAGTGAAGTGAAGTGAAGT	11640		
Db	51028	GAGATGAAGATCATTAAGATCAATTAAGACAGCTGTAAAGTGAAGTGAAGTGAAGT	51087		
QY	11641	AAGCAAGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	11700		
Db	51088	AAGCAAGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	51147		
QY	11701	TTTTAATTTACTGTTGGAACCTTAATTTTCTTTTAACTGAAAGAAAGCTGTGCTGAT	11760		
Db	51148	TTTTAATTTACTGTTGGAACCTTAATTTTCTTTTAACTGAAAGAAAGCTGTGCTGAT	51207		
QY	11761	GACTTAAGTGTTCAGCTGTTAATTTTGAAGACTTGACAGTCAAGATGATGATGATGAT	11820		
Db	51208	GACTTAAGTGTTCAGCTGTTAATTTTGAAGACTTGACAGTCAAGATGATGATGATGAT	51267		
QY	11821	CTTCTTGGAAAGTGTGTTGTTTATTTATTTACCTTTTGAAGTGTGCAAAAAAACAC	11880		
Db	51268	CTTCTTGGAAAGTGTGTTGTTTATTTATTTACCTTTTGAAGTGTGCAAAAAAACAC	51327		
QY	11881	TACATATTTGATGCTGTAGTAAAGATGATGATGATGATGATGATGATGATGATGAT	11940		
Db	51328	TACATATTTGATGCTGTAGTAAAGATGATGATGATGATGATGATGATGATGATGAT	51387		
QY	11941	CAATCCTATGACCTTTGAGAAATGAACCTTATAGGCTTTCAGAGAGGATTCAGAGAG	12000		
Db	51388	CAATCCTATGACCTTTGAGAAATGAACCTTATAGGCTTTCAGAGAGGATTCAGAGAG	51447		
QY	12001	GCATGACGCAAAACATTTGTCGCCAGTGTGGAAGCATTAATTTTCTCTTAAGATT	12060		
Db	51448	GCATGACGCAAAACATTTGTCGCCAGTGTGGAAGCATTAATTTTCTCTTAAGATT	51507		
QY	12061	TTTTTTAGCTTCTGCGAGTATTTATCCTCTTTAGGGAAGATGTAACAGAGTAA	12120		
Db	51508	TTTTTTAGCTTCTGCGAGTATTTATCCTCTTTAGGGAAGATGTAACAGAGTAA	51567		
QY	12121	AGAAATTAAGGCTCAGACCTCATCTGAGTATGTTTCTTAAGCATTAATGATGCTGT	12180		
Db	51568	AGAAATTAAGGCTCAGACCTCATCTGAGTATGTTTCTTAAGCATTAATGATGCTGT	51627		
QY	12181	GCTTTTAATTAATTTAGTGAATGATTAATGATTAATTAATGATGATGATGATGATGAT	12240		
Db	51628	GCTTTTAATTAATTTAGTGAATGATTAATGATTAATTAATGATGATGATGATGATGAT	51687		
QY	12241	GACTACAAAAGTGTGCTGACGTAAGCATCCCTTATTTGAATTTGCTTTTCTGTA	12300		
Db	51688	GACTACAAAAGTGTGCTGACGTAAGCATCCCTTATTTGAATTTGCTTTTCTGTA	51747		
QY	12301	TCACCTGCCATTTCTTTAGAAAAAGAACATCTTGGAGAGTGGGCTCCATTCATT	12360		
Db	51748	TCACCTGCCATTTCTTTAGAAAAAGAACATCTTGGAGAGTGGGCTCCATTCATT	51807		
QY	12361	GAGGAAGAGAGTATTAACAAAGAACACAGAGAGAGTGAAGAGCCCTGTATAT	12420		
Db	51808	GAGGAAGAGAGTATTAACAAAGAACACAGAGAGAGTGAAGAGCCCTGTATAT	51867		
QY	12421	TAGTCACAGTATCTTTTACACAGAGATTAATGATTTCTTAGGATTAATTTTATAT	12480		

Db	47488	AAAAAGGAATATATACATATACCGCGGGCGTGGTGCCTCACGCTCTGTAATCCACCACCTTTG	47547
Qy	8101	GGAGGCTGAGCGCGCGGATCACCTGAGCTCAGGAGTTGGAGACCCAGCTGACATAACATG	8160
Db	47548	GGAGGCTGAGCGCGCGGATCACCTGAGCTCAGGAGTTGGAGACCCAGCTGACATAACATG	47607
Qy	8161	GAGAAACCCCATCTCTACTAAATACAAATATAGCCAGAGTGGTGACACATGCCTGTA	8220
Db	47608	GAGAAACCCCATCTCTACTAAATACAAATATAGCCAGAGTGGTGACACATGCCTGTA	47667
Qy	8221	ATCCAGCTACTCCGGAGGCTGAGCGAGGAGATTCGCTTCAACTGGGAGGCGAGAGTTG	8280
Db	47668	ATCCAGCTACTCCGGAGGCTGAGCGAGGAGATTCGCTTCAACTGGGAGGCGAGAGTTG	47727
Qy	8281	CGGTGAGCGAGATTCGCGCGCTTGGCGCTCCATCCTGGGCGACAAAGGCAAACTCCATCT	8340
Db	47728	CGGTGAGCGAGATTCGCGCGCTTGGCGCTCCATCCTGGGCGACAAAGGCAAACTCCATCT	47787
Qy	8341	CAAAAAAGAAATATACATAGCATATAGAAATATACATATATATATATATAG	8400
Db	47788	CAAAAAAGAAATATACATAGCATATAGAAATATACATATATATATATATATAG	47847
Qy	8401	AAATATACATACGTACACATATATACATTCCTTATGTGTTAACTTTCTTTATAGTT	8460
Db	47848	AAATATACATACGTACACATATATACATTCCTTATGTGTTAACTTTCTTTATAGTT	47907
Qy	8461	TCTCTCCCTCTCTTTTTTTTTTTTCTTTCGCAATATATGTTAACTTTCTTTATAGTT	8520
Db	47908	TCTCTCCCTCTCTTTTTTTTTTTTCTTTCGCAATATATGTTAACTTTCTTTATAGTT	47967
Qy	8521	TGGCTCATACCTGTAATCCAGCATTTTGGGAGCGGAGTGGGCGGATCACCTGAGTTC	8580
Db	47968	TGGCTCATACCTGTAATCCAGCATTTTGGGAGCGGAGTGGGCGGATCACCTGAGTTC	48027
Qy	8581	AGGAGTTTGGCAACCGGCTGGCCAGCATGGTGAACCTTTGTCCTATTAATAATAGAAAA	8640
Db	48028	AGGAGTTTGGCAACCGGCTGGCCAGCATGGTGAACCTTTGTCCTATTAATAATAGAAAA	48087
Qy	8641	ATTAGCTGGGTGTTGATGTCGCTGTAATCCAGCTACTCAGGAGCGTGAAGGAGGA	8700
Db	48088	ATTAGCTGGGTGTTGATGTCGCTGTAATCCAGCTACTCAGGAGCGTGAAGGAGGA	48147
Qy	8701	GAATCGCTTGAACCCAGGAGGAGTTCATCTCAAAAAAAGAGAGAGAGAGGA	8820
Db	48148	GAATCGCTTGAACCCAGGAGGAGTTCATCTCAAAAAAAGAGAGAGAGAGGA	8827
Qy	8761	AGCTCGGTCACAGACGGAGATTCATCTCAAAAAAAGAGAGAGAGAGGA	8820
Db	48208	AGCTCGGTCACAGACGGAGATTCATCTCAAAAAAAGAGAGAGAGAGGA	48267
Qy	8821	GAAGAAGAACCCAGCTTACCTGTAGAAATTTCCACCTCTAGATTCGATCTGTGTT	8880
Db	48268	GAAGAAGAACCCAGCTTACCTGTAGAAATTTCCACCTCTAGATTCGATCTGTGTT	48327
Qy	8881	ATTATTAACATGTTCCCTATTTCCCTATTTCCCTATTTCCCTATTTCCCTATTTCCCT	8940
Db	48328	ATTATTAACATGTTCCCTATTTCCCTATTTCCCTATTTCCCTATTTCCCTATTTCCCT	48387
Qy	8941	ACTTGATAGGATCAAAATTTGATTTGTCGTGAGGAAATCTTTATGGCTAGTGGGTA	9000
Db	48388	ACTTGATAGGATCAAAATTTGATTTGTCGTGAGGAAATCTTTATGGCTAGTGGGTA	48447
Qy	9001	CTTCTATTAGGAGCAGATATGTCGTGTTGTTCTCTTTTCTGTCATCTGTCAGCCATTT	9060
Db	48448	CTTCTATTAGGAGCAGATATGTCGTGTTGTTCTCTTTTCTGTCATCTGTCAGCCATTT	48507
Qy	9061	AATGATAATTCCTAGGCTGTTATTAATGAGGTTGATAAAAATTTGATAAATCTAAT	9120
Db	48508	AATGATAATTCCTAGGCTGTTATTAATGAGGTTGATAAAAATTTGATAAATCTAAT	48567
Qy	9121	TCTATCATTTATTAATTCATAGGATATTTCTTAATAGAAATTCCTCCCTCATCAATTTG	9180
Db	48568	TCTATCATTTATTAATTCATAGGATATTTCTTAATAGAAATTCCTCCCTCATCAATTTG	48627
Qy	9181	TATGGATATATTTGGGGAACAGTTTACACAGAAAGGCATATAAATGCTTGAATCTTTTC	9240
Db	48628	TATGGATATATTTGGGGAACAGTTTACACAGAAAGGCATATAAATGCTTGAATCTTTTC	48687
Qy	9241	ATTTTTTTTTTACCCTTACTAAAGAGTTGGTTCTGTTAGCATCTCTTCAAGAGTGAAAA	9300
Db	48688	ATTTTTTTTTTACCCTTACTAAAGAGTTGGTTCTGTTAGCATCTCTTCAAGAGTGAAAA	48747
Qy	9301	ATGAACCTTTTGTGTTGTTGTTCCAGTAATTTCTAAATGTCATCCCTTCAAGAACCATTT	9360
Db	48748	ATGAACCTTTTGTGTTGTTGTTCCAGTAATTTCTAAATGTCATCCCTTCAAGAACCATTT	48807
Qy	9361	GTATTTGGTTCTTTCTTCTAGTTGAGTTCAGGTTGATGATCCAGCATGATTGTTGTCATATG	9420
Db	48808	GTATTTGGTTCTTTCTTCTAGTTGAGTTCAGGTTGATGATCCAGCATGATTGTTGTCATATG	48867
Qy	9421	TACTTGGAGCTTTCCGCTCACCTGCTGTTGATATAAGTATATTTGTCATTTCTAGGTTTC	9480
Db	48868	TACTTGGAGCTTTCCGCTCACCTGCTGTTGATATAAGTATATTTGTCATTTCTAGGTTTC	48927
Qy	9481	ACCTAGAAATCAATGACCCAAAGCTCATTTCAAGAGGAAGCAGATAGTCTTTCAGATA	9540
Db	48928	ACCTAGAAATCAATGACCCAAAGCTCATTTCAAGAGGAAGCAGATAGTCTTTCAGATA	48987
Qy	9541	GTGGACAGGCGAGCTATGAACAAATTTGGACCTTGGAGTTCAGTTCAGTTCATTTCAAT	9600
Db	48988	GTGGACAGGCGAGCTATGAACAAATTTGGACCTTGGAGTTCAGTTCAGTTCATTTCAAT	49047
Qy	9601	TTTATTTTGAAGTATAGTTGGGAGCTCAGTTGTAAGTATGATTGGATTGATTTCATTT	9660
Db	49048	TTTATTTTGAAGTATAGTTGGGAGCTCAGTTGTAAGTATGATTGGATTGATTTCATTT	49107
Qy	9661	ATTCCTTCTGATTTATACATTTATTAATGCCCCCATCTTATTTGTTTATTTATATAAAG	9720
Db	49108	ATTCCTTCTGATTTATACATTTATTAATGCCCCCATCTTATTTGTTTATTTATATAAAG	49167
Qy	9721	CAAAATAACAGTGTGTTACCTTTTGAACATATGTTTATTTGTTTATTTATATAAAG	9780
Db	49168	CAAAATAACAGTGTGTTACCTTTTGAACATATGTTTATTTGTTTATTTATATAAAG	49227
Qy	9781	ACCATATGCTGCTGTTTATTCATCTCATATAATAAAGAAATTTTAAACACCTGCCGG	9840
Db	49228	ACCATATGCTGCTGTTTATTCATCTCATATAATAAAGAAATTTTAAACACCTGCCGG	49287
Qy	9841	AGGTTAGAACAACTTTTACACATTTGATAATACGTTAAATTTACATTTCCAGTAAGAGAC	9900
Db	49288	AGGTTAGAACAACTTTTACACATTTGATAATACGTTAAATTTACATTTCCAGTAAGAGAC	49347
Qy	9901	ATTTTCCCGAGGAAATGTTTTTCAAAATGTTATTTTATGTTTCTGTTGCTACATCAG	9960
Db	49348	ATTTTCCCGAGGAAATGTTTTTCAAAATGTTATTTTATGTTTCTGTTGCTACATCAG	49407
Qy	9961	TCTTAAACAGTAGTCACCTTAATTTTCAAAATGTTATATATATATATATATATTTT	10020
Db	49408	TCTTAAACAGTAGTCACCTTAATTTTCAAAATGTTATATATATATATATATATATTTT	49467
Qy	10021	TGAGGAGTGTGGGAGTGGAGGAGATCAATGATGGTATATATATAAAGAAATTTGTT	10080
Db	49468	TGAGGAGTGTGGGAGTGGAGGAGATCAATGATGGTATATATATAAAGAAATTTGTT	49527
Qy	10081	TCCTCCAGATTCAGATGAAGAGATTTTGTAAAGTAAAGTGTGAAAAACAGGAGTTCT	10140
Db	49528	TCCTCCAGATTCAGATGAAGAGATTTTGTAAAGTAAAGTGTGAAAAACAGGAGTTCT	49587
Qy	10141	ACAAGACAGTATTTCCGAAACAGAGGACACAAATGCTCTCCAGAGAAATACCTATGA	10200
Db	49588	ACAAGACAGTATTTCCGAAACAGAGGACACAAATGCTCTCCAGAGAAATACCTATGA	49647
Qy	10201	CAGTCCCGAGGAGGAAATTAAGAGATTTTATATGCTGGGAAAAATACAAAAATCAAAAG	10260
Db	49648	CAGTCCCGAGGAGGAAATTAAGAGATTTTATATGCTGGGAAAAATACAAAAATCAAAAG	49707

QY 5881 AATGTTATTCATTTGATTTACTGAATTTTGTGAGACCTCCACCACCCCTGTTACTGGCC 5940  
| | | | |  
Db 45338 AATGTTATTCATTTGATTTACTGAATTTTGTGAGACCTCCACCACCCCTGTTACTGGCC 45387  
| | | | |  
QY 5941 TGCCCTTGAGCTGCTGCTGAAATTTGCTAGAGATTAATGCTATTCAAGACCCCTATT 6000  
| | | | |  
Db 45388 TGCCCTTGAGCTGCTGCTGAAATTTGCTAGAGATTAATGCTATTCAAGACCCCTATT 45447  
| | | | |  
QY 6001 CCTTGAGCTGCTGCTGAAATTTGCTTCCACACTCCACAAACAGAGTAATAGTTT 6060  
| | | | |  
Db 45448 CCTTGAGCTGCTGCTGAAATTTGCTTCCACACTCCACAAACAGAGTAATAGTTT 45507  
| | | | |  
QY 6061 TACTGCTTTGATTTGTTAGAGATCATCAGTGCATATATTATTCTGACCAATCCCA 6120  
| | | | |  
Db 45508 TACTGCTTTGATTTGTTAGAGATCATCAGTGCATATATTATTCTGACCAATCCCA 45567  
| | | | |  
QY 6121 GCACCTTGAGAGCTGAAGCCCGGAGATTGCTTGAGCTCAGAGTTCCAAACACCTGAC 6180  
| | | | |  
Db 45568 GCACCTTGAGAGCTGAAGCCCGGAGATTGCTTGAGCTCAGAGTTCCAAACACCTGAC 45627  
| | | | |  
QY 6181 ATAGAAAACATGGCAAAACCCCGCTCTACAAAACAAAAAATTAAGCGGGCGTCCGCT 6240  
| | | | |  
Db 45628 ATAGAAAACATGGCAAAACCCCGCTCTACAAAACAAAAAATTAAGCGGGCGTCCGCT 45687  
| | | | |  
QY 6241 GTGGTCCCAAGCTACTGCTCCAGCTACTGGGGTGGTGAAGAGTAATCCTTTGGGC 6300  
| | | | |  
Db 45688 GTGGTCCCAAGCTACTGCTCCAGCTACTGGGGTGGTGAAGAGTAATCCTTTGGGC 45747  
| | | | |  
QY 6301 CTGGAGGCTCAAGGCTGAGTGAGATGCTCCCACTGCACTCCAGCCGCTGAGTGA 6360  
| | | | |  
Db 45748 CTGGAGGCTCAAGGCTGAGTGAGATGCTCCCACTGCACTCCAGCCGCTGAGTGA 45807  
| | | | |  
QY 6361 GAGTGAGACACTGTATCAAAAAAATTTTGTACCTTGCAATTAATCAATTTAT 6420  
| | | | |  
Db 45808 GAGTGAGACACTGTATCAAAAAAATTTTGTACCTTGCAATTAATCAATTTAT 45867  
| | | | |  
QY 6421 AATTTTTTTTTTTGAGAGGAGTCTGCTCTGTGCCCCAGACTGGAGTGGAC 6480  
| | | | |  
Db 45868 AATTTTTTTTTTTGAGAGGAGTCTGCTCTGTGCCCCAGACTGGAGTGGAC 45927  
| | | | |  
QY 6481 AATCTCGGCTCACTGCACTCTGCTCTGCTGATTCAGACGATTTCTCGCCCCAGCTC 6540  
| | | | |  
Db 45928 AATCTCGGCTCACTGCACTCTGCTCTGCTGATTCAGACGATTTCTCGCCCCAGCTC 45987  
| | | | |  
QY 6541 CTGAGCAGCTGGGACTACAGGACACACACACCCAGCTAATTTTTGTATTTTAT 6600  
| | | | |  
Db 45988 CTGAGCAGCTGGGACTACAGGACACACACACCCAGCTAATTTTTGTATTTTAT 46047  
| | | | |  
QY 6601 AGATACGGGGTTTACTGCTATTTGGCCAGGCTAGTCTCAACTCTGACCTGTTGATTCAC 6660  
| | | | |  
Db 46048 AGATACGGGGTTTACTGCTATTTGGCCAGGCTAGTCTCAACTCTGACCTGTTGATTCAC 46107  
| | | | |  
QY 6661 CCACCTCGGCTCCCAAAAGTCTGGGATTTACAGGCGTGAGCCACCATGCGACCAATTT 6720  
| | | | |  
Db 46108 CCACCTCGGCTCCCAAAAGTCTGGGATTTACAGGCGTGAGCCACCATGCGACCAATTT 46167  
| | | | |  
QY 6721 AATATTTTTTTGACAAACCACTCAGCTGAGGCTGCTGCTGTTACTATTAATGATGTTTC 6780  
| | | | |  
Db 46168 AATATTTTTTTGACAAACCACTCAGCTGAGGCTGCTGCTGTTACTATTAATGATGTTTC 46227  
| | | | |  
QY 6781 AATATTTCCCTTTATTAATTAAGTTGATTCAGAGCCCTGAGAAACACTAAGAGGTAGCT 6840  
| | | | |  
Db 46228 AATATTTCCCTTTATTAATTAAGTTGATTCAGAGCCCTGAGAAACACTAAGAGGTAGCT 46287  
| | | | |  
QY 6841 TGCGATCTAGGCTTAGCTTTAAGGTCACTAAGTCAAGTCACTAAGCAACCCCTCTCT 6900  
| | | | |  
Db 46288 TGCGATCTAGGCTTAGCTTTAAGGTCACTAAGTCAAGTCACTAAGCAACCCCTCTCT 46347  
| | | | |  
QY 6901 CCTTAGCTTTTATTTGCGACTTTTAAAGTCTTATTTAGAAATTTTCAACCTATAC 6960  
| | | | |  
Db 46348 CCTTAGCTTTTATTTGCGACTTTTAAAGTCTTATTTAGAAATTTTCAACCTATAC 46407  
| | | | |  
QY 6961 AACCGTAGAAGGATGATTAATTAACCCATCACTTACTCACTAGTGTGAATATC 7020  
| | | | |

Db 46408 AACCGTAGAAGGATGATTAATTAACCCATCACTTACTCACTAGTGTGAATATC 46467  
| | | | |  
QY 7021 TCTGCTGCAATGCTTGGAGCCAGAACGCTTTTGAATTTGATTCATTTTGCATTTTG 7080  
| | | | |  
Db 46468 TCTGCTGCAATGCTTGGAGCCAGAACGCTTTTGAATTTGATTCATTTTGCATTTTG 46527  
| | | | |  
QY 7081 GAATTTTGGCATACATTAAGAGTATCTTTGGGGAGGAGCCCAAGTCTAAACATGAA 7140  
| | | | |  
Db 46528 GAATTTTGGCATACATTAAGAGTATCTTTGGGGAGGAGCCCAAGTCTAAACATGAA 46587  
| | | | |  
QY 7141 TTCACTATATTTTCAATATACCTTACACATATGCTGAAAGTATTTTATACAGATT 7200  
| | | | |  
Db 46588 TTCACTATATTTTCAATATACCTTACACATATGCTGAAAGTATTTTATACAGATT 46647  
| | | | |  
QY 7201 TTAATAATATTTGCTGATGAAGCAAAAGTTTACTGCAAGCTCATATAGGTGACGT 7260  
| | | | |  
Db 46648 TTAATAATATTTGCTGATGAAGCAAAAGTTTACTGCAAGCTCATATAGGTGACGT 46707  
| | | | |  
QY 7261 GTGGAATTTTCACTAGTGGCATCATCTGAGTCTCAAAATTTTGGAAATTTGGAGCAT 7320  
| | | | |  
Db 46708 GTGGAATTTTCACTAGTGGCATCATCTGAGTCTCAAAATTTTGGAAATTTGGAGCAT 46767  
| | | | |  
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Db	43168	AGAAATTAAGATTATCAACCAATATTTTGGTATCTGAGCAGCCACAAAATTTT	43227	QY	4861	GAGCGCTGCTCTCCGGCTGAGGGAATCAGAGACAGCTCCGTCCTCTAGTGGAGCGGAGG	4920
QY	3781	TTTCTTTAGAGACAAGTCTCCCTCTATCGCTACGCTGAAGTGCAGTGGTGGATCAT	3840	Db	44308	GAGCGCTGCTCTCCGGCTGAGGGAATCAGAGACAGCTCCGTCCTCTAGTGGAGCGGAGG	44367
Db	43228	TTTCTTTAGAGACAAGTCTCCCTCTATCGCTACGCTGAAGTGCAGTGGTGGATCAT	43287	QY	4921	GAGCGAAGTCTATGACAGCGGAGTGGTCTTCTGAGTGAAGTTCATGACACACGCCCCCA	4980
QY	3841	ACTCACTCTAACCTCAAACTCCCTGGACTAAGCCATCTCCACCTCGGCTCCCAAGC	3900	Db	44368	GAGCGAAGTCTATGACAGCGGAGTGGTCTTCTGAGTGAAGTTCATGACACACGCCCCCA	44427
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Db	43348	GTTCAGATTACAAGCGTGAAGCATGAGAGCGCGGCTCTTTTAAAAATAAAGTGGGCGG	43407	QY	5041	CCGAGCGCGCGGCGGAGGACTGCGGCTCCCGGCTTCGCGCGCGGCTCCCGCGG	5100
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Db	43408	GGCAGAGTGGCTCACGCTCTGAGGGTATGAGGCTTCGAGCAGCTTCGAGCGCGGAGG	43467	QY	5101	CTCAGACTCGGCGCGGATGGGTTCCGACCGGCAATCCCGTCCCGCGCGGCGGCTTC	5160
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Db	43468	CGAGGATCATTTGAGATCAGGAGTTCGAGACCGAGCTTCGAGCAGCTTCGAGCGCGG	43527	QY	5161	CGCTTCGGGCTCGTGGCGGAGAGCTCCAGGTTCTCTGGGCGCGGCACTGCGCGGAGCC	5220
QY	4081	TCTACTAAAAATACAAAATTTAGCCAGGGTTCGAGGCTTCGAGCAGCTTCGAGCGG	4140	Db	44608	CGCTTCGGGCTCGTGGCGGAGAGCTCCAGGTTCTCTGGGCGCGGCACTGCGCGGAGCC	44667
Db	43528	TCTACTAAAAATACAAAATTTAGCCAGGGTTCGAGGCTTCGAGCAGCTTCGAGCGG	43587	QY	5221	AGCCCTCTTCAGCGCGGTTCTGCGCGGAGGCTCCCTCTTCGCGCGGCTTCCTGTGCGG	5280
QY	4141	TCAGGAGGTGAGGCGACGAGAACTCGCTTGAACCGGAGGCGGAGGTTGAGCGGCGG	4200	Db	44668	AGCCCTCTTCAGCGCGGTTCTGCGCGGAGGCTCCCTCTTCGCGCGGCTTCCTGTGCGG	44727
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QY	4201	GATCGCGGCTCATCTTCCTGCTGCTAACAGAGGAGACTCCATCTCAAAAAA	4260	Db	44728	AGCTCTCTCCCTCAGGCTGCTGAAAGCGGAGGCTCTAGCCGAGGCTTCAGCCGAGCC	44787
Db	43648	GATCGCGGCTCATCTTCCTGCTGCTAACAGAGGAGACTCCATCTCAAAAAA	43707	QY	5341	GGTGGCGGGGATTCCTCCGAGAGAGGCGGAGGCTGTAGGAGTTCACACACTG	5400
QY	4261	AAGTGTGTGTATACATACATATGTATGTATATATATATATATATATATATATAT	4320	Db	44788	GGTGGCGGGGATTCCTCCGAGAGAGGCGGAGGCTGTAGGAGTTCACACACTG	44847
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QY	4321	ACATATGTGTGTGTATATATATATATATATATATATATATATATATATATATAT	4380	Db	44848	GGCTGGGAGGCGCTCGAGGCTATCGCGCGGAGGCTTCGCGCGGAGGCTTCGCGGAGG	44907
Db	43768	ACATATGTGTGTGTATATATATATATATATATATATATATATATATATATATAT	43827	QY	5461	CCGAGTGGGAAAGTCAACCGCTCGGCTGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCT	5520
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Db	43888	TCAGTGGGAAATCCCGGAGGAACTTGGAAATTCCTCTAAAAAGTTCAGGTACAGGAC	43947	QY	5581	CACCTCCGCTTAGGAGCAAAATTTAAAGGCGGCGCAAAACCTCAATCAAACTCATAT	5640
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QY	4561	AATCGCAGTGTGCTTGGCAGTGTCAAGGTCAAGGTCAGGCTCGCTGGTACCG	4620	Db	45088	TTAATGCAATATTTTAAAAAACCAAAATTAATGCAAAACCTTTTATGATTTGATTTG	45147
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QY	4621	ACTGCCCGCCCGCTGCACTTCAGCTCCCGGAGGCTCCGCTACGAGGCTGCGACCC	4680	Db	45148	ACAAAATATCAGAGCTTTAAACAAAGAGAGATCGGACAGCTTTTACAAAACCGGG	45207
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QY	4741	CGGAAGGGGGGAGCTCGCTGGAAGGCCCCCTCTGGATTGGTGCAAAACCATCTGGGT	4800	Db	45268	CATATTTTACCTCATGAGCTGTAGATTATTTTAAATTTTAAATAATATTGCAATT	45327
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		DB	39868	TGTTTTCTAGTTTACAAAAAGAACAGATTTCTTTCTTTTTTGAATGGAGTCTTGCTC	39927
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		DB	39928	TGTCACCCAGGCTGGAGTGCAGTGGTGACAGATCTCAGCTCACCACAATCTCCGCTCCC	39987
		QY	541	AGGTTCAAGCAATTTCTCTGCCTCAGCCTCCCAAGTAGCTGGGACTCAGAGTGGCCGCA	600
		DB	39988	AGGTTCAAGCAATTTCTCTGCCTCAGCCTCCCAAGTAGCTGGGACTCAGAGTGGCCGCA	40047
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		DB	40108	TGGTCTCAAACTCTCGGCTCAAGTGATCTGACTGCGCTCAGCCTCCCAAAATCTGGGAT	40167
		QY	721	TACAGGCATGACCCACTCACCCACCAACCTCCAAAAAAGAACACATTTCTCGAAAACTAAAT	780
		DB	40168	TACAGGCATGACCCACTCACCCACCAACCTCCAAAAAAGAACACATTTCTCGAAAACTAAAT	40227
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		DB	40228	TAGTTACCTAAGTTTATGAAGCCCTCTATGGAGCAGGTTTCAGACTTAATCCCTGTAAAGTG	40287
		QY	841	AGCACTCCAGATGTTTCTCTTTGTTGCCATTATCAACTTGTATAACAAGGATTGTTGGAT	900
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		QY	1021	ACTTTATCTTGGCACAAGTTAATGTGTAAATAAAAGTTTCTCGGGATGGAGGAGTAT	1080
		DB	40468	ACTTTATCTTGGCACAAGTTAATGTGTAAATAAAAGTTTCTCGGGATGGAGGAGTAT	40527
		QY	1081	GAAAGTTGTTCTTAATGGGCATAGAGTTTTCAGTTTTCGAAGATCAAAAGAGTCTTAGGCC	1140
		DB	40528	GAAAGTTGTTCTTAATGGGCATAGAGTTTTCAGTTTTCGAAGATCAAAAGAGTCTTAGGCC	40587
		QY	1141	AGGCCCTGGGTGCACACCTGTAATTCACAGCGCTTTGGGAGGCCAGGTCATGGGTCAC	1200
		DB	40588	AGGCCCTGGGTGCACACCTGTAATTCACAGCGCTTTGGGAGGCCAGGTCATGGGTCAC	40647
		QY	1201	TTGAGGTCAGAGTTCAAGACTAGCCTGGCCCAACATGGTGAACCCCGCTCTCTCTAAGA	1260
		DB	40648	TTGAGGTCAGAGTTCAAGACTAGCCTGGCCCAACATGGTGAACCCCGCTCTCTCTAAGA	40707
		QY	1261	ATACATACAAAAAGTAGCCAGGCGTGTGGCAGTGCCTGTATATCCACGCTACTTGGGA	1320
		DB	40708	ATACATACAAAAAGTAGCCAGGCGTGTGGCAGTGCCTGTATATCCACGCTACTTGGGA	40767
		QY	1321	GGCTGAGGCAGGAGAATTTGCTTGAACCCGGGAGGCAGAGGTTGCAGTGCAGCAAGATAGC	1380
		DB	40768	GGCTGAGGCAGGAGAATTTGCTTGAACCCGGGAGGCAGAGGTTGCAGTGCAGCAAGATAGC	40827
		QY	1381	ACCATTGCTTCCAGCCTAGGCAACAGAGCAAACTCCATTTCAAAAAAAGAGAG	1440
		DB	40828	ACCATTGCTTCCAGCCTAGGCAACAGAGCAAACTCCATTTCAAAAAAAGAGAG	40887
		QY	1441	AGAAAAAGAAAGAAATTTCTGAAGATTCGATGTTGTTTACATACAAATTTGAATGTACTT	1500
		DB	40888	AGAAAAAGAAAGAAATTTCTGAAGATTCGATGTTGTTTACATACAAATTTGAATGTACTT	40947



**AUTHORS** Howden, P.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (06-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk; Clone Requests: clonerequests@sanger.ac.uk  
**COMMENT** On Sep 19, 2000 this sequence version replaced gi:9714820. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/projects/c\\_elegans/wormpep](http://www.sanger.ac.uk/projects/c_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>

This sequence is the entire insert of clone RP11-43507. The true left end of clone RP1-6283 is at 123829 in this sequence. The true right end of clone RP4-555823 is at 81044 in this sequence. This sequence has been finished according to sequence map criteria as follows: An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-43507 is from the library RPCR-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
**VECTOR:** pBAC3.6

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 47814..47877  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 14:54:01 ; Search time 48642 Seconds  
(without alignments)  
17949.183 Million cell updates/sec

Title: US-09-982-091A-5\_COPY\_1\_30000  
Perfect score: 30000  
Sequence: 1 aagcaggtagtttaactt.....taataaaaaataagaatgacc 30000

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*

1: gb.ba:\*  
2: gb.htg:\*  
3: gb.in:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vi:\*  
15: em.ba:\*  
16: em.fun:\*  
17: em.hum:\*  
18: em.in:\*  
19: em.mu:\*  
20: em.om:\*  
21: em.or:\*  
22: em.ov:\*  
23: em.pat:\*  
24: em.ph:\*  
25: em.pl:\*  
26: em.ro:\*  
27: em.sts:\*  
28: em.un:\*  
29: em.vi:\*  
30: em.htg\_hum:\*  
31: em.htg\_inv:\*  
32: em.htg\_other:\*  
33: em.htg\_mus:\*  
34: em.htg\_pln:\*  
35: em.htg\_rod:\*  
36: em.htg\_vrt:\*  
37: em.htg\_mam:\*  
38: em.sy:\*  
39: em.htgo\_hum:\*  
40: em.htgo\_mus:\*  
41: em.htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	25833	86.1	194296	9	AL354864	AL354864 Human DNA
2	10530	35.1	111862	2	AL139143	AL139143 Homo sapi
3	575	1.9	4756	9	AF297866	AF297866 Homo sapi
c	487	1.6	193690	2	AC118559	AC118559 Homo sapi
5	231	0.8	421	6	AX246208	AX246208 Sequence
6	173	0.7	422	6	AX246209	AX246209 Sequence
7	173	0.6	393	6	AX245923	AX245923 Sequence
8	164	0.5	408	6	AX245847	AX245847 Sequence
9	138	0.5	411	6	AX071922	AX071922 Sequence
10	135	0.4	386	6	AX069706	AX069706 Sequence
11	133	0.4	406	6	AX071923	AX071923 Sequence
12	113	0.4	174562	2	AC005848	AC005848 Homo sapi
13	112	0.4	221475	9	AC009562	AC009562 Homo sapi
14	109	0.4	127661	2	AP001261	AP001261 Homo sapi
15	109	0.4	160535	9	AP000729	AP000729 Homo sapi
c	109	0.4	199522	9	AC089999	AC089999 Homo sapi
17	106	0.4	164684	9	AL590683	AL590683 Human DNA
c	105	0.4	38897	9	AC021092	AC021092 Homo sapi
18	105	0.4	156321	9	AC074331	AC074331 Homo sapi
c	104	0.3	43507	9	AF305057	AF305057 Homo sapi
20	104	0.3	152711	9	AP001178	AP001178 Homo sapi
21	104	0.3	147250	2	AC011778	AC011778 Homo sapi
c	103	0.3	177743	9	AC105941	AC105941 Homo sapi
23	103	0.3	189441	2	AC022989	AC022989 Homo sapi
24	103	0.3	89251	9	HS03812P3	AL121909 Human DNA
25	102	0.3	139118	9	AL133477	AL133477 Human DNA
26	101	0.3	166584	9	AC015922	AC015922 Homo sapi
27	101	0.3	185415	9	HS121M24	AL354046 Homo sapi
c	101	0.3	164306	2	AP002785	AP002785 Homo sapi
29	99	0.3	170172	2	AC104765	AC104765 Homo sapi
c	99	0.3	187190	2	AC026898	AC026898 Homo sapi
31	99	0.3	308676	2	AC068639	AC068639 Homo sapi
c	98	0.3	131753	9	AL358790	AL358790 Human DNA
33	97	0.3	151445	9	AL354943	AL354943 Human DNA
34	97	0.3	160460	2	AC024374	AC024374 Homo sapi
c	97	0.3	161536	2	AC024318	AC024318 Homo sapi
36	97	0.3	167981	2	AL591856	AL591856 Homo sapi
37	97	0.3	169089	9	AC008537	AC008537 Homo sapi
c	97	0.3	173758	9	AC009144	AC009144 Homo sapi
39	97	0.3	192016	2	AC026540	AC026540 Homo sapi
c	97	0.3	216215	9	HSG256022	AL080239 Human DNA
41	97	0.3	237613	2	AC025769	AC025769 Homo sapi
c	97	0.3	72045	9	AC092214	AC092214 Homo sapi
43	96	0.3	103056	9	AC068447	AC068447 Homo sapi
44	96	0.3	104794	9	AC104046	AC104046 Homo sapi
c	96	0.3	104794	9	AC104046	AC104046 Homo sapi

# ALIGNMENTS

RESULT 1  
AL354864  
LOCUS  
DEFINITION  
Human DNA sequence from clone RP11-435D7 on chromosome 1. Contains ESTs, STSS, GSSs and CpG islands. Contains a novel gene and the 5' part of the PSMB2 gene for proteasome (prosome, macropain) subunit 2, beta type, complete sequence.  
ACCESSION  
AL354864  
VERSION  
AL354864.16 GI:10185566  
KEYWORDS  
HTG; CpG island; macropain; prosome; proteasome; PSMB2.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 194296)

Db 415 GTGGTCTGGCAGCTCTGCTCCCTCTGGAGACAACGGCTATGCCAGCTTCCTCTGA 474  
 QY 28837 G 28837  
 Db 475 G 475

RESULT 6  
 AX333105/c  
 LOCUS AX333105 466 bp DNA Linear PAT 09-JAN-2002  
 DEFINITION Sequence 3614 from Patent WO0194629.  
 ACCESSION AX333105  
 VERSION AX333105.1 GI:18123739  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,  
 Horrigan, S., Soppet, D.R. and Weaver, Z.  
 TITLE Cancer gene determination and therapeutic screening using signature  
 gene sets  
 JOURNAL Patent: WO 0194629-A 3614 13-DEC-2001;  
 Avalon Pharmaceuticals (US)  
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 BASE COUNT 143 a 90 c 103 g 129 t 1 others  
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Query Match 1.2%; Score 340; DB 6; Length 466;  
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 QY 9549 CTCTAATTTTCTGGGCTTGGGATGAAGATAAGTGTACACCCAGTGTTCGCCACCA 9608  
 Db 280 CTCTAATTTTCTGGGCTTGGGATGAAGATAAGTGTACACCCAGTGTTCGCCACCA 221  
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 QY 9669 TCAAGATCTCCCTCTGGGCTGTCGACAGAAGAAACATAACCCCTTATTTGCAATCTT 9728  
 Db 160 TCAAGATCTCCCTCTGGGCTGTCGACAGAAGAAACATAACCCCTTATTTGCAATCTT 101  
 QY 9729 CTGGCTTACATACATTTGCCCTCACTAATCAATGGACATTTTCAGCATTTTACTAATTT 9788  
 Db 100 CTGGCTTACATACATTTGCCCTCACTAATCAATGGACATTTTCAGCATTTTACTAATTT 41  
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 Db 40 TGAGAAGGCCACCACCATGGAATTTAATAAAATATTATTG 1

RESULT 7  
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 LOCUS G30470 466 bp DNA Linear STS 05-OCT-1996  
 DEFINITION human STS SHGC-37119, sequence tagged site.  
 ACCESSION G30470  
 VERSION G30470.1 GI:1594021  
 KEYWORDS STS; STS sequence; primer; sequence tagged site.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 466)

# AUTHORS JOURNAL COMMENT

Myers, R. M.  
 Unpublished (1996)

Contact: Richard M. Myers  
 Stanford Human Genome Center (SHGC)  
 Stanford University School of Medicine  
 Department of Genetics, M-344, Stanford, CA 94305, USA  
 Tel: 4157259687  
 Fax: 4157259689  
 Email: myers@shgc.stanford.edu

Primer A: TTTATTAATTCATGTTGGCC  
 Primer B: CCTTCTGGTCTGACAA  
 STS size: 140  
 PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds  
 Annealing: 62 degrees C for 23 seconds  
 Polymerization: 72 degrees C for 30 seconds  
 PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:  
 Template: 25 ng  
 Primer: each 1 uM  
 dNTPs: each 200 uM  
 Taq Polymerase: 0.05 units/ul  
 Total Vol: 10 ul

Buffer:  
 MgCl2: 2.5 mM  
 KCl: 50 mM  
 Tris-HCl: 20 mM  
 pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from N72576  
 -- Washington University/Merck EST sequence.

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 /db\_xref="taxon:9606"  
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Best Local Similarity 100.0%; Pred. No. 1e-164;

Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 340 GAATTAATTTTCTGCTCTTAATAAGGACTTAACTGGTACCCCAAGTCAGAAAGACTCTGC 281

QY 9549 CTCTAATTTTCTGGGCTTGGGATGAAGATAAGTGTACACCCAGTGTTCGCCACCA 9608

Db 280 CTCTAATTTTCTGGGCTTGGGATGAAGATAAGTGTACACCCAGTGTTCGCCACCA 221

QY 9609 CAGCTGTGGGCGAGAGACCCCTTCTGGGACTGAATTTCTCAATTTGAAGCACTGTGT 9668

Db 220 CAGCTGTGGGCGAGAGACCCCTTCTGGGACTGAATTTCTCAATTTGAAGCACTGTGT 161

QY 9669 TCAAGATCTCCCTCTGGGCTGTCGACAGAAGAAACATAACCCCTTATTTGCAATCTT 9728

Db 160 TCAAGATCTCCCTCTGGGCTGTCGACAGAAGAAACATAACCCCTTATTTGCAATCTT 101

QY 9729 CTGGCTTACATACATTTGCCCTCACTAATCAATGGACATTTTCAGCATTTTACTAATTT 9788

Db 100 CTGGCTTACATACATTTGCCCTCACTAATCAATGGACATTTTCAGCATTTTACTAATTT 41

QY 9789 TGAGAAGGCCACCACCATGGAATTTAATAAAATATTATTG 9828

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LOCUS  
DEFINITION Homo sapiens cDNA FLJ39147 f1s, clone OCBBF200523.  
ACCESSION AK096466  
VERSION AK096466.1 GI:21755971  
KEYWORDS oligo cloning; fls (full insert sequence).  
SOURCE Homo sapiens fetal brain cDNA to mRNA, clone\_11b:OCBFR2  
clone:OCBFR200523.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hirooka, S.,  
Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,  
Sugiyama, T., Irie, K., Otsuki, T., Sato, H., Ota, T., Makamatsu, A.,  
Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K.,  
Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M.,  
Kikuchi, H., Kanda, K., Magatsuma, M., Takahashi-Fujii, A., Oshima, A.,  
Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K.,  
Masuo, Y., Nagai, K. and Isogai, T.  
TITLE NEDO human cDNA sequencing project  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2394)  
AUTHORS Isogai, T. and Yamamoto, J.  
TITLE Direct Submission  
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FII Project (HRI Team); 2-6-7  
Kazusa-kamatarai, Kisarazu, Chiba 392-0812, Japan (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction: Helix Research Institute (HRI) (supported by Japan  
Key Technology Center etc.); 5'-6 3'-end one pass sequencing: RAB,  
HRI, and Biotechnology Center, National Institute of Technology and  
Evaluation; clone selection for full insert sequencing: HRI and  
RAB; annotation: HRI and RAB.  
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Best Local Similarity 100.0%; Pred No. 1.8e-143;  
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 128 AGCTCCTGAGTACACCGCTTGACAAACAGAGCCCTTGATCCCTGAGGA 187  
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OY 28719 GGGTGGCAGAGCCCCCAGAGGGGCGAGAGATTCCTGGGGCTGAGAGATGGCT 28778  
|||||  
Db 188 GGGGTGGCAGAGCCCCCAGAGGGGCGAGAGATTCCTGGGGCTGAGAGATGGCT 247  
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OY 28779 GGTGCTGGCAGAGTGGCTCCCTCTGGAGGAGCAAGGCTATGCCAGAGTCCCTGAG 28837  
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Db 248 GGTGCTGGCAGAGTGGCTCCCTCTGGAGGAGCAAGGCTATGCCAGAGTCCCTGAG 306  
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RESULT 9  
AF297866 4756 bp mRNA linear PRI 21-OCT-2000  
LOCUS  
DEFINITION Homo sapiens Hu-Claspilin mRNA, complete cds.  
ACCESSION AF297866  
VERSION AF297866.1 GI:10944333  
KEYWORDS  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Kumagai, A. and Dunphy, W.G.  
TITLE 1 (bases 1 to 4756)  
JOURNAL Mol. Cell 6 (4), 839-845 (2000)  
MEDLINE 21000493  
JOURNAL 11090622  
REFERENCE 2 (bases 1 to 4756)  
AUTHORS Kumagai, A. and Dunphy, W.G.  
TITLE Direct Submission  
JOURNAL Submitted (21-AUG-2000) Biology, California Institute of  
Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA  
FEATURES  
source  
Location/Qualifiers  
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TAGKAKVSKRLKEKERMERIKRLKKEKTEKNOEDVQEPFNDGCLLVKDTLETG  
LEDENNSPLEDESESLIRAAKYNKVKHKKKEPELSEGVSEEGSLSGTTRKER  
KAARLSKRLKQHSRTORLIRBSALNIPYHNEPKTIHDFPKRPRPTCKGNMALL  
KSKYSSHHKEDIPTATPMKNSHHKSGSQTTGAENVEFTNALPYVSKETQITIG  
SDPSRKDLVNEELIEOKQSDIRSPGSSVLOOESVFLGNHSEECQVGLVA  
FEPALBEQEPNPEETDEKEEPOOKSSAVGPEVRRRTLDRLQOLCVDSIKP  
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FEPALALCSGSPPTDKDEDEDEEGFRLVSNDESDSDDEHSDGNDLAFLLN  
EDGSEEEDEEEMTDESEDEEKEVEKEEELKEEGGKEEKEEGNGOETAFLL  
SSEELIETDKEMDKENNDGSEEGKAGVGLSPKSLSDSTLLLFKSSKMGCSPT  
PEKSTDENSGCOPKLEDDSCSLITRESHNSFELIGTISYQCNKOTGKTS  
FFPTAGRSRSPGFLRSLVSSAKSSGKSESPLEDSODLYNASPEKTLTGA  
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CTGKFTSOAEKHLPRKSDRKEMBELNLKCSGKPSODASTPASSELKORKESSMG  
PMEEALALCSGSPPTDKDEDEDEEGFRLVSNDESDSDDEHSDGNDLAFLLN  
DDDEELIETDKEMDKENNDGSEEGKAGVGLSPKSLSDSTLLLFKSSKMGCSPT  
PSDELOQIKTIHMKTYLDDDKRLRLIROYETIACGLHSDGPOKMRPKMKNIDA  
SOMDLFVHSDDDQJTEOULDESEAKRERIEREQLMDMAQOQKVTAESEEGSDS  
QOMILAKRVYDAALOKNARSRPVYIDESSLRNPEALRPSAOVKRTSLNPKAV  
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## ORIGIN

Query Match 1.0%; Score 291; DB 9; Length 4756;  
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 Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db TCAGAAGATCCACAGAGAGGACTCTGACTGGCTCACCTGGAGTGGAGCTCTATCCCTGG 4045

QY 23879 ATTCTTCAGGCTTCATTTGACCCACATGTTAAGCTGGGAGACAGACTCCAAAGAGA 23938  
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QY 23939 GCCGAGAGAGGCTTATCTGGGAGAGAAACAATGATGACTTTATGGCTCTGTGGTCT 23998  
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QY 23999 GGGCAGAACTGCATAACCTAGATCACCAAGCTGAGAGCTTTAGAGTGGAGTTGG 24058  
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 Db GGGCAGAACTGCATAACCTAGATCACCAAGCTGAGAGCTTTAGAGTGGAGTTGG 4225

QY 24059 GCCAGGATGGTGGCTCACGCCCTGTAATCCAGCAGCTTTGGGAGCGAGCTGGTGGAT 24118  
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 Db GCCAGGATGGTGGCTCACGCCCTGTAATCCAGCAGCTTTGGGAGCGAGCTGGTGGAT 4285

QY 24119 CACAAGCTCAGGAGATCAACACCAACCTGACCAACATGGTGA 24160  
 |||||  
 Db CACAAGCTCAGGAGATCAACACCAACCTGACCAACATGGTGA 4327

## RESULT 10

AC099686 111744 bp DNA linear HTG 21-AUG-2002  
 LOCUS Homo sapiens chromosome 15 clone CTD-2052B23 map 15, WORKING DRAFT  
 DEFINITION AC099686  
 SEQUENCE AC099686  
 VERSION AC099686.2 GI:22380845  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 111744)  
 Birren,B., Nusbaum,C. and Lander,E.  
 Homo sapiens chromosome 15, clone CTD-2052B23  
 Unpublished  
 2 (bases 1 to 111744)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,  
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,  
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,  
 Cooke,P., DeAtrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,  
 Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,  
 Glinde,S., Gord,S., Goyette,M., Graham,L., Hulme,W., Iliev,I., Johnson,R.,  
 Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K.,  
 Lamazares,R., Landers,T., Lechoczky,J., Levine,R., Liu,G.,  
 Maclean,C., Macdonald,P., McKernan,K., McPheeters,R., Meldrim,J.,  
 McCarthy,M., McEwan,P., McKernan,K., Marquis,N., Matthews,C.,  
 Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,  
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,  
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,  
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,  
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,  
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (18-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

Submitted (18-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE  
AUTHORS

3 (bases 1 to 111744)  
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
 Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,  
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,  
 Cook,A., Cooke,P., DeAtrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
 Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,  
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,  
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,  
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 McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,  
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 Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,  
 Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Aug 21, 2002 this sequence version replaced gi:16974178.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

## TITLE

## JOURNAL

## COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WBIR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu

Project Information  
 Center project name: L12850  
 Center clone name: 2052\_B\_23

Summary Statistics  
 Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 110017 bases at least Q40  
 Consensus quality: 110530 bases at least Q30  
 Consensus quality: 110909 bases at least Q20  
 Insert size: 109000; agarose-fp  
 Insert size: 111344; sum-of-contigs  
 Quality coverage: 22.6 in Q20 bases; agarose-fp  
 Quality coverage: 22.1 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently  
 consists of 5 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 6251: contig of 6251 bp in length  
 6252 6351: gap of 100 bp  
 6352 24838: contig of 18487 bp in length  
 24839 24938: gap of 100 bp  
 24939 42760: contig of 17822 bp in length  
 42761 42860: gap of 100 bp  
 42861 67794: contig of 24934 bp in length  
 67795 67894: gap of 100 bp  
 67895 111744: contig of 43850 bp in length.

Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /chromosome="15"  
 /map="15"  
 /clone.lib="CITD1 Human BAC"  
 1. 6251  
 /note="assembly\_fragment"

FEATURES  
 source  
 misc\_feature  
 1. 6251

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WtBR  
 Web site: <http://www.seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 Project Information  
 Center project name: L6262  
 Center clone name: 635\_O\_13

1	1309:	contlg of	1309 bp	in length
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1410	24262:	contlg of	1053 bp	in length
2463	2562:	gap of	100 bp	
2563	3707:	contlg of	1145 bp	in length
3708	3807:	gap of	100 bp	
3808	4998:	contlg of	1191 bp	in length
4999	5098:	gap of	100 bp	
5099	6927:	contlg of	1829 bp	in length
6928	7027:	gap of	100 bp	
7028	8933:	contlg of	1906 bp	in length
8934	9033:	gap of	100 bp	
9034	10733:	contlg of	1700 bp	in length
10734	10833:	gap of	100 bp	
10834	12128:	contlg of	1295 bp	in length
12129	12228:	gap of	100 bp	
12229	14227:	contlg of	1999 bp	in length
14228	14327:	gap of	100 bp	
14328	16144:	contlg of	1817 bp	in length
16145	16244:	gap of	100 bp	
16245	17544:	contlg of	1300 bp	in length
17545	17644:	gap of	100 bp	
17645	19728:	contlg of	2084 bp	in length
19728	19828:	gap of	100 bp	
19829	21896:	contlg of	2068 bp	in length
21897	21996:	gap of	100 bp	
21997	23660:	contlg of	1664 bp	in length
23661	23760:	gap of	100 bp	
23761	27013:	contlg of	3253 bp	in length
27014	27113:	gap of	100 bp	
27114	29667:	contlg of	2554 bp	in length
29668	29767:	gap of	100 bp	
29768	33523:	contlg of	2756 bp	in length
33524	32623:	gap of	100 bp	
32624	36050:	contlg of	3427 bp	in length
36051	36150:	gap of	100 bp	
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37489	37588:	gap of	100 bp	
37589	40082:	contlg of	2494 bp	in length
40083	40182:	gap of	100 bp	
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43509	46386:	contlg of	2878 bp	in length
46387	46486:	gap of	100 bp	
46487	50157:	contlg of	3671 bp	in length
50158	50257:	gap of	100 bp	
50258	55228:	contlg of	2971 bp	in length
53229	53328:	gap of	100 bp	
53329	56167:	contlg of	2839 bp	in length
56168	56267:	gap of	100 bp	
56268	61644:	contlg of	5377 bp	in length
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61745	65196:	contlg of	3452 bp	in length

\* 65197 65296: gap of 100 bp  
 \* 65297 70157: contig of 4861 bp in length  
 \* 70158 70257: gap of 100 bp  
 \* 70258 74554: contig of 4297 bp in length  
 \* 74555 74654: gap of 100 bp  
 \* 74655 79228: contig of 4574 bp in length  
 \* 79229 79328: gap of 100 bp  
 \* 79329 84640: contig of 5312 bp in length  
 \* 84641 84740: gap of 100 bp  
 \* 84741 89974: contig of 5234 bp in length  
 \* 89975 90074: gap of 100 bp  
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 \* 96884 96983: gap of 100 bp  
 \* 96984 102058: contig of 5075 bp in length  
 \* 102059 102158: gap of 100 bp  
 \* 102159 107640: contig of 5482 bp in length  
 \* 107641 107740: gap of 100 bp  
 \* 107741 113941: contig of 6201 bp in length  
 \* 113942 114041: gap of 100 bp  
 \* 114042 118500: contig of 4459 bp in length  
 \* 118501 118600: gap of 100 bp  
 \* 118601 125732: contig of 7132 bp in length  
 \* 125733 125832: gap of 100 bp  
 \* 125833 132596: contig of 6764 bp in length  
 \* 132597 132696: gap of 100 bp  
 \* 132697 139895: contig of 7199 bp in length  
 \* 139896 147426: contig of 7431 bp in length  
 \* 147427 147526: gap of 100 bp  
 \* 147527 153241: contig of 5715 bp in length  
 \* 153242 153341: gap of 100 bp  
 \* 153342 161613: contig of 8272 bp in length.

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1. .1309  
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misc\_feature

1410. .2462  
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12229. .14227  
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 Db 107016 CCAACATGGTGAACCCCATCTCTACTAAATAACAAAAATTAGC 106972

## RESULT 12

AC092450.4

## WPCOMMENT

Sequence split into 8 fragments LOCUS AC092450 Accession AC092450

Fragment Name	Begin	End
AC092450_0	1	110000
AC092450_1	100001	210000
AC092450_2	200001	310000
AC092450_3	300001	410000
AC092450_4	400001	510000
AC092450_5	500001	610000
AC092450_6	600001	710000
AC092450_7	700001	727300

Continuation (5 of 8) of AC092450 from base 400001 (AC092450 Homo sapiens chromosome

Query Match 0.9%; Score 246; DB 2; Length 110000;  
 Best Local Similarity 100.0%; Pred. No. 5e-116;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24149 CCAACATGGTGAACCCCATCTCTACTAAATAACAAAAATTAGCTG 24195  
 |||||  
 Db 39351 CCAACATGGTGAACCCCATCTCTACTAAATAACAAAAATTAGCTG 39397

## RESULT 13

AC092450.6/c

## WPCOMMENT

Sequence split into 8 fragments LOCUS AC092450 Accession AC092450

Fragment Name	Begin	End
AC092450_0	1	110000
AC092450_1	100001	210000
AC092450_2	200001	310000
AC092450_3	300001	410000
AC092450_4	400001	510000
AC092450_5	500001	610000
AC092450_6	600001	710000
AC092450_7	700001	727300

Continuation (7 of 8) of AC092450 from base 600001 (AC092450 Homo sapiens chromosome

Query Match 0.9%; Score 246; DB 2; Length 110000;  
 Best Local Similarity 100.0%; Pred. No. 5e-116;  
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 |||||  
 Db 88212 TCTTGGCTCACTGCAACCTCCACCTCCAGGTTCAAGCGATTCTCTGCTCAGGCTCCC 88153

## RESULT 14

HSJ231P7P/c

## LOCUS

HSJ231P7P 80485 bp DNA linear PRI 26-JUL-1999

DEFINITION Human DNA sequence from clone 231P7P on chromosome 22q11.21-12.2

Contains CA repeat and STS, complete sequence.

ACCESSION AL096757

VERSION AL096757.1 GI:5420250

KEYWORDS HTG: repeat polymorphism.

SOURCE Homo sapiens.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1 (bases 1 to 80485)
AUTHORS Corby,N.
TITLE Direct Submission
JOURNAL Submitted (26-Jul-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
COMMENT During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
variation annotation may not be found in the sequence submission
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 22, constructed by the Sanger Centre Chromosome 22
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22
231P/P is from the library Rpci1 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://pacpac.med.buffalo.edu/VECTOR: pCYPAC2 This
sequence is the entire insert of clone 231P/P.
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2247..2312
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2451..2486
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2840..2890
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3454..3493
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3693..3742
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4091..4150
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5099..5150
/note="26 copies 2 mer ca 96% conserved"
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5280..5343
/note="2 copies 32 mer 91% conserved"
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5284..5343
/note="15 copies 4 mer ca 97% conserved"
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5284..5341
/note="29 copies 2 mer ca 98% conserved"
repeat_region
5344..5637
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repeat_region
5687..5897
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5926..6013
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6469..6733
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7892..8202
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8262..8454
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repeat_region
10128..10489
/note="L2 repeat: matches 1768..2187 of consensus"
repeat_region
10559..10644
/note="43 copies 2 mer cc 63% conserved"
repeat_region
10755..10917
/note="L2 repeat: matches 2543..2710 of consensus"
repeat_region
11250..11287
/note="L1PA8 repeat: matches 5953..5990 of consensus"
repeat_region
11361..11663
/note="AluSx repeat: matches 1..295 of consensus"
repeat_region
11679..11786
/note="MIR repeat: matches 21..147 of consensus"
repeat_region
12268..12395
/note="MIR repeat: matches 118..262 of consensus"
repeat_region
12723..12774
/note="MIR repeat: matches 210..261 of consensus"
repeat_region
12779..12818
/note="10 copies 4 mer acac 93% conserved"
repeat_region
12779..12816
/note="19 copies 2 mer ac 95% conserved"
repeat_region
13045..13151
/note="MER91C repeat: matches 1..119 of consensus"
repeat_region
13227..13530
/note="AluY repeat: matches 1..304 of consensus"
repeat_region
13997..14081
/note="MIR repeat: matches 53..139 of consensus"
repeat_region
14935..14998
/note="MIR repeat: matches 80..144 of consensus"
repeat_region
15852..15891
/note="20 copies 2 mer gt 93% conserved"
repeat_region
15945..16336
/note="L2 repeat: matches 2095..2490 of consensus"
repeat_region
16883..17092
/note="MIR repeat: matches 39..252 of consensus"
repeat_region
17787..18087
/note="AluSx repeat: matches 2..303 of consensus"
repeat_region
18342..18505
/note="MIR repeat: matches 103..262 of consensus"
repeat_region
18879..19024
/note="MIR repeat: matches 47..197 of consensus"
repeat_region
19560..19815
/note="2 copies 128 mer 80% conserved"
repeat_region
20108..20306
/note="MIR repeat: matches 47..260 of consensus"
repeat_region
20430..20615
/note="L2 repeat: matches 2308..2498 of consensus"
repeat_region
20902..20986
/note="MIR repeat: matches 107..192 of consensus"
repeat_region
22071..22138
/note="MIR repeat: matches 77..146 of consensus"

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repeat_region 22319..22418
/note="AluY repeat: matches 202..302 of consensus"
repeat_region 22474..22735
/note="L2 repeat: matches 2469..2750 of consensus"
repeat_region 22736..23023
/note="AluSp repeat: matches 1..289 of consensus"
repeat_region 23024..23042
/note="L2 repeat: matches 2453..2469 of consensus"
repeat_region 23412..23504
/note="MIR repeat: matches 46..143 of consensus"
repeat_region 23905..24045
/note="47 copies 3 mer atg 89% conserved"
repeat_region 23907..24290
/note="3 copies 128 mer 78% conserved"
repeat_region 24050..24151
/note="34 copies 3 mer gat 80% conserved"
repeat_region 24991..25077
/note="MIR repeat: matches 47..143 of consensus"
repeat_region 25282..25458
/note="L2 repeat: matches 2264..2418 of consensus"
repeat_region 25563..25957
/note="MSTO repeat: matches 1..394 of consensus"
repeat_region 26295..26604
/note="LIME1 repeat: matches 5505..5826 of consensus"
repeat_region 26705..26855
/note="L2 repeat: matches 2588..2749 of consensus"
repeat_region 26901..26972
/note="18 copies 4 mer gatg 72% conserved"
repeat_region 27383..27676
/note="AluX repeat: matches 1..296 of consensus"
repeat_region 27678..27854
/note="MIR repeat: matches 67..257 of consensus"
repeat_region 28123..28190
/note="MIR repeat: matches 109..183 of consensus"
repeat_region 28597..28750
/note="L2 repeat: matches 2591..2750 of consensus"
repeat_region 30377..30691
/note="AluDo repeat: matches 1..309 of consensus"
repeat_region 30692..31007
/note="MER47A repeat: matches 49..366 of consensus"
repeat_region 31452..31588
/note="MIR repeat: matches 46..192 of consensus"
repeat_region 31843..31902
/note="30 copies 2 mer ca 68% conserved"

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Db 61164 ACAGTGGCTCAGCGCTGTAATCCAGCACTTTGGGAGGCCAAGGC 61120

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## RESULT 15

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 LOCUS Homo sapiens chromosome 19 clone LLNLR-269B9, complete sequence.  
 DEFINITION AC008999  
 ACCESSION AC008999  
 VERSION AC008999.7 GI:15281189

KEYWORDS HTG.  
 SOURCE Homo sapiens.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 39707)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
 TITLE Direct Submission  
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 39707)  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Direct Submission

JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint

REFERENCE 3 (bases 1 to 39707)  
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 4 (bases 1 to 39707)  
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 5 (bases 1 to 39707)  
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 On Aug 23, 2001 this sequence version replaced gi:11079409.  
 Draft Sequence Produced by DOE Joint Genome Institute  
 www.jgi.doe.gov

COMMENTS  
 Finishing Completed at Stanford Human Genome Center  
 www-shgc.stanford.edu  
 Quality: Phrap Quality >=40 100% of Sequence;  
 Estimated Total Number of Errors is 0.

## FEATURES

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Db 8469 GGAGCTGAGCGAGGAGGAGTTCCTTGAACCCGGAGGTGAGGTTGC 8515

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 Job time : 92791 secs